OM protein - protein search, using sw model

November 25, 2002, 02:52:20; Search time 51 Seconds (without alignments) 857.670 Million cell updates/sec Run on:

US-09-825-751A-20 2447 1 MDFPRVLLSAVFLISFLWDL.......GNNVVYKQYEDMVVESCGCR 455 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283224 seqs, 96134422 residues Searched:

283224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	cartilage-derived	qrowth/differentia	bone morphogenetic	cartilage-derived	bone morphogenetic		bone morphogenetic	bone morphogenetic	SPDVR1 protein - s	bone morphogenetic	bone morphogenetic		bone morphogenetic	bone morphogenetic	osteogenic protein	bone morphogenetic	osteogenic protein	decapentaplegic pr	Vg-1-related prote										
SUMMARIES	ΩI	B55452	JC2347	S43294	A55452	S43295	543296	JH0687	JH0688	I50608	BMHU4	149541	S37073	S38343	BMHU2	S52408	JH0801	S45355	S58791	I49542	150607	A45056	BMHU5	JH0689	A49147	об90нг	ВМНU7	JQ1184	A26158	A54798
	DB	7	N	~	7	7	7	~	7	ď	Н	7	7	~	-	~	7	7	7	~	~	~		7	~	~	Т	~	~	7
	Length	436	501	495	501	125	151	398	398	405	408	420	393	408	396	461	408	. 394	408	452	353	402	454	401	400	426	431	430	588	510
aР	Query	73.5	37.9	37.6	37.5	æ	22.4	19.2	19.0	18.5	18.0	17.8	17.7	17.7	17.6	17.6	•	٠	17.1	17.1	17.1	17.0	17.0	16.9	16.7	•	16.4	•	٠	
	Score	1798	927.5	919.5	918.5	691	549	470	464	453	441.5	436.5	m	432.5		429.5	426.5	423	419.5	418.5	417.5	416.5	416.5	413.5	408.5	407	401.5	401	395.5	394.5
	Result No.		7	e	4	2	9	7	æ	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	22	56	27	28	29

bone morphogenetic	bone morphogenetic	qene nodal protein	TGF beta homolog d	bone morphogenetic	bone morphogenetic	cet-1 protein - Ca	TGF-beta-related p	vqr protein - rat	bone morphogenetic	Vql embryonic grow	GDF-1 embryonic gr	inhibin beta-A cha	inhibin beta-A cha	inhibin beta-A cha	inhibin beta-A cha
BMHU6	151284	S29718	A40735	JC4646	JC4838	T43286	A43918	S37618	BMHU3	A29619	C39364	B24248	I47072 *	WFPGBA	850898
7	7	~	7	7	7	~	7	7	-	7	7	Н	~	П	٦
513	313	354	427	476	478	365	455	207	472	360	372	426	425	424	425
16.1	16.0	15.4	15.2	14.3	14.3	14.0	14.0	13.6	13.3	13.3	13.1	13.0	12.8	12.7	12.5
			~1	_	5.	43	343	334	5.5	4.5	9.5	318	3.5	310	6.5
	391	377	373	35	350	m	٠.,		32	32	31		31		30

ALIGNMENTS

) 2000 /ba, N.J.P.; Ko transforming gr 190	Gaps 8;	86 61	146 121	206 179	265 239	317 299	377 358	437 418	
RESULT 1 B55452 cartillage-derived morphogenetic protein 2 precursor - bovine (fragment) cartillage-derived morphogenetic protein 2 precursor - bovine (fragment) C;Species: Bos primigenius taurus (cattle) C;Date: 10-Feb-1995 #sequence_revision 10-Feb-1995 #text_change 26-May-2000 C;Accession: B55452 R;Chang, S.C.: Hoang, B.; Thomas, J.T.; Vukicevic, S.; Luyten, F.P.; Ryba, N.J.P.; A;Title: Cartilage-derived morphogenetic proteins. New members of the transforming A;Accession: B55452 A;Accession: B55452 A;Accession: B55452 A;Scatus: preliminary; not compared with conceptual translation A;Molecule type: mRNA A;Residues: 1-436 - CARA> A;Cross-references: GB:U13661; NID:g632489; PIDN:AAA61416.1; PID:g632490 C;Superfamily: inhibin); Score 1798; DB 2; Length 436; 5; Pred. No. 8.1e-120; 18; Mismatches 48; Indels 18;	SSAELGSTKGMRSRKEGKWQRAPRDSDAGREGQEPQPRPQDEPRAQQPRAQEPP 	GRGPRVVPHEYMLSIYRIYSIAEKLGINASFPQSSKSANTITSFVDRGLDDLSHTPLRRQ 	WGPPAGPLHVQLFPCLSPLLLDARTLDPQG 	APPAGWEVEDVWQGLRHQPWKQLCLELRAAM-GELDAGEAEARARGPQQPPPPDLRSLGF 	GRRVRPPQERALLVVFTRSQRKNLFAEMREQLGSA-EAAGPGAGAEGSWPPPS	GAPDARPWLPSPGRRRRTAFASRHGKRHGKKSRLRCSKKPLHVNFKELGWDDWIIAPLE 	YEAYHCEGVCDFPLRSHLEPTNHAIIQTLMNSMDPGSTPPSCCVPTKLFPISILXIDAGN . 	155
RESULT 1 B55452 cartilage-derived morphogenet C;Species: Bos primigenius ta C;Date: 10-Feb-1995 #sequence C;Accession: B55452 R;Chang, S.C.; Hoang, B.; Tho A;Title: Cartilage-derived mo A;Reference number: A55452 A;Tetle: Cartilage-derived mo A;Reference number: A55452 A;Status: prellminary; not co A;Molecule type: mRNA A;Residues: 1-436 < CHA> A;Cross-references: GB:113661 C;Superfamily: inhibin	Query Match 73.5%; Best Local Similarity 80.8%; Matches 354; Conservative 1				APPAGWEVFDVWQGLRHQP APRPGWEVFDVWRGLRPQP				NVVYKQYEDMVVESCGCR 455 : : NVVYNEYEEMVVESCGCR 436
RESULT 1 B55452 cartilage C, Species C, Species C, Accessig R, Chang, J, Biol. A, Title: A, Referen A, Referen A, Roleculs A, Roleculs A, Roleculs A, Roleculs C, Superfau C, Superfau	Query Match Best Local Matches 35	Qy 33 Db 2	Qy 87 Db 62	Qy 147 Db 122	Oy 207 Db 180	Oy 266 Db 240	Qy 318 Db 300	Qy 378 Db 359	Oy 438 Db. 419

PID:9488462

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GB:U08337; NID:g488461; PIDN:AAA18778.1;
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-495 <STO>
A;Cross-references: GB:UG
C;Superfamily: inhibin
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A: Residues: 1-501 < CHA>
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                                                                            C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 17-Mar-2000
C; Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 17-Mar-2000
C; Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 17-Mar-2000
C; Neckerian G: Neidhardt, H.; Jacobowsky, B.; Pohl, J.
Biochem. Biophys. Res. Commun. 204, 646-652, 1994
A; Title: Cloning and expression of recombinant human growth/differentiation factor 5.
A; Reference number: JC2347; MUID:95071375; PMID:7980526
A; Molecule type: DNA
A; Residues: 1-501 AHOE>
A; Molecule type: DNA
A; Residues: 1-501 AHOE>
A; Cross-references: GB: X80915; NID:9671524; PIDN:CAA56874.1; PID:9671525
A; Genetics: A; Genetics: A; Genetics: GB: A; A; Introns: 21/1
C; Superfamily: inhibin
C; Reywords: glycoprotein
F; 189/Binding site: carbohydrate (Asn) (covalent) #status predicted
F; 381-382/Cleavage site: Arg-Ala (unidentified proteinase) #status predicted
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A;Title: Limb alterations in brachypodism mice due to mutations in a new member A;Reference number: S43294; MUID:94195427; PMID:8145850
A;Accession: S43294
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C;Species: Mus musculus (house mouse)
C;Date: 20-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 17-Mar-2000
C;Accession: S43294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              97;
                                                                                                                                                                                                                                                                                                                                                                                                                            Length 501;
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                                                                                                                                                                                                                                                                                                                                                                                                                          37.9%; Score 927.5; DB 2;
44.7%; Pred. No. 3.6e-58;
iive 64; Mismatches 98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38 GSTKGMRSRKEGKMQRAPRDSDAGREGQEPQPRPQDEPRAQQ--
                                                                 growth/differentiation factor 5 - human
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Matches 209; Conservative
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F.P.; Ryba, N.J.P.;
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                                               18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cartilage-derived morphogenetic protein 1 precursor - human C.Species: Homo sapiens (man) C.Date: 10-Feb-1995 #sequence_revision 10-Feb-1995 #text_change 17-Mar-2000 C;Accession: A55452 Hoang, B.: Thomas, J.T.; Vukicevic, S.; Luyten, F.P.; Ryba, N.J. Biol. Chem. 269, 28227-28234, 1994. Arritle: Cartilage-derived morphogenetic proteins. New members of the transf A.Reference number: A55452 MUID:95050604; PMID:7961761 A.Accession: A55452 A.Status: preliminary
                                                                                                                     217 VWQGLRH-QPWKQLCLELRAAWGELDAGEAEARARGPQQPPPPDLRSLGFGRRVRPPQER 275
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                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALLVVFTRSQRKNL-FAEMREQLGSAEAAGPGAGAEGSWPPPSGAPDARPWLPSPGRRRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----PRAQQP------RAQEP------PGRGPRVVPHEYMLSIYRT
                                                                                                                                                                                                                                                                105 YSIAEKLGINASFFQSSKSANTITSFVDRGLDDLSHTPLRRQKYLFDVSMLSDKEELVGA
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                                             91;
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    Length 495;
                                               Indels
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37.6%; Score 919.5; DB 2;
43.5%; Pred. No. 1.3e-57;
iive 74; Mismatches 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 918.5; DB 2;
Pred. No. 1.5e-57;
4; Mismatches 101;
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                        Best Local Similarity 43.59
Matches 209; Conservative
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C; Date: 20-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 19-May-2000 C; Accession: S43296 R; Storm, E.E.; Huynh, T.V.; Copeland, N.G.; Jenkins, N.A.; Kingsley, D.M.; Lee, S.J. Nature 368, 639-643, 1994 A; Title: Limb alterations in brachypodism mice due to mutations in a new member of the A; Reference number: S43294; MUID:94195427; PMID:8145850	A; Accession: \$4326 A; Status: preliminary A; Molecule type: DNA A; Residues: 1-151 <sto> A; Cross-references: GB: U08339; NID: 9488465; PIDN: AAA18780.1; PID: 9488466 C; Superfamily: inhibin</sto>	Query Match 22.4%; Score 549; DB 2; Length 151; Best Local Similarity 59.5%; Pred. No. 5.9e-32; Matches 103; Conservative 13; Mismatches 35; Indels 22; Gaps 1; Qy 283 RSQRKNLFAEMREQLGSAEAAGPGAGAEGSWPPPSGAPDARPWLPSPGRRRRTAFASRH 342	QY 34.3 GKRHGKKSRLRCSKKPLHVNFKELGWDDWIIAPLEYEAYHCEGVCDFPLRSHLEPTNHAI 402 1: : : :	PRESULT 7 JOHNS TO COME TO The Construction of the Company of the
81 GQTGGLTQPKKDEPKKLPPRPG-GPEPKPGHPPQTRQATARTVTPKGQLPGGKAP 13 80PRAQEPPGRGPRVVPHEYMLSIXRTYSIAEKLGINASFFQ 11 135 PKAGSVPSSFLLKKAREPGPPREPKEPFRPPITPHEYMLSLYRTLSDADRKGGNSSVKL 19	OY 120 SSEANTIEFFUNGLDUDSHIPLEKONILEHUVSMLSDKEELVGARELKLEKGAPSAFWGF 1/9 195 EAGLANTIEFFUNGQDDRGPV-VRKQRVVFDISAL-EKDGLLGAELRILRKKPS-DTAK 251 QY 180 PAGPLHVQLFPCLSPLLLDARTLDPQGAPPAGWEVFDVWQGLRH-QPWKQL 229 DA 250 DAVDBSDDANOITE SCHOOLDART PAGE CHARACTERISTICAL STANDARD 250	230 CLELRAAMGELDAGEARARGPQOPPPDDLRSLGFGRRVRPPQERALLVVFTRSQRKNL	349 KSRLRCSKRPLHVNFKELGWDWIIAPLEYE 349 KSRLRCSKRALHVNFKELGWDWIIAPLEYE 395 NLKARCSRKALHVNFKDMGWDDWIIAPLEYE 409 SWDPGSTPPSCCVPTKLTPISILYIDAGNNV	RESULT 5 843295 bone morphogenetic protein homolog GDF6 precursor - mouse (fragment) Nathernate names: growth and differentiation factor 6 C:Specia: Nus musculus (house mouse) C:Date: 20-oct.1994 #sequence_revision 07-Feb-1997 #text_change 26-May-2000 C:Date: 20-oct.1994 #sequence_revision 07-Feb-1997 #text_change 26-May-2000 C:Accession: 843295 R:Storm. E.E.: Huyth, T.V.: Copeland, N.G.: Jenkins, N.A.: Kingsley, D.M.: Lee, S.J. Natite: Lima alterations in brachypodism mice due to mutations in a new member of the TA:Title: Lima alterations in brachypodism mice due to mutations in a new member of the TA:Title: Lima alterations in brachypodism mice due to mutations in a new member of the TA:Title: Lima alterations in brachypodism mice due to mutations in a new member of the TA:Title: Lima alterations in brachypodism mice due to mutations in a new member of the TA:Title: Lima alterations in brachypodism mice due to mutations in a new member of the TA:Title: Lima alterations in brachypodism mice due to mutations in a new member of the TA:Title: Lima alterations in brachypodism mice due to mutations in a new member of the TA:Title: Lima alterations in brachypodism mice due to mutations in a new member of the TA:Title: Lima alterations in brachypodism mice due to mutations in a new member of the TA:Title: Lima alterations in polybasic protease recognition site #status predicted cp: Superior alterated protein (GDF7) - mouse Oy 331 RRRRPARARAERIC protein-related protein (GDF7) - mouse RESULT 6 Bone morphogenetic protein-related protein (GDF7) - mouse

A; Gene: GDB: BMP4; BMP2B A; Cross-references: GDB:125205;	RESULT 9
A; Residues: 1-408 <wo3> A; Residues: 1-408 <wo3> A; Cross-references: GB:M22490; N</wo3></wo3>	Db 360 KACCVPTELSAISMLYINGDBWVEGGGCR 398
A; Reference number: A37278; MUI. A; Accession: C37278	100
Science 242, 1528-1534, 1988 A; Title: Novel regulators of bo	Qy 357 KPLHVNFKELGWDDWIIAPLEYEAYHCEGVCDFPLRSHLEPTNHAIIQTLANSMDPGSTP 416 Db 301 HPIYVDFSTNGWINMTVAPDGYHARVCHRFORFPLAHLAYGANTAYNGYMT MSCNMT AIG 360
C;Date: 16-Sep-1992 #sequence_r C;Accession: C37278 R:Woznev J M : Rosen V : Cele	Db 273GKGHALH
N, Alternate names: bone morphog C; Species: Homo sapiens (man)	299 SAEAAGPGAGAEGSWPPPSGAPDARPWLPSFGRRRRTFTAFASRHGKKSRLRCSK
RESULT 10 BMHU4 bone morphogenetic protein 4 pr	OY 243 GEAEARARGPQOPPPDLRSLGFGRRVRPPQERALLVVFTRSQRKNLFAEMREQLG 298 1
DD 348 STNHALVQTLVNSVN-SSIPKP	OY 196LLDARTLDPQGAPPAGWEVFDVWQGLRHQPWKQLCLELRAAWGELDA 242
Db 288 RARRSPKHHGSRKNKKNCRRHA	of the day of the day of the control
Qy 338 FASRHGKRHG-KKSRLRCSKKF	OS FIFGANNY IFFIMLULI HLHSAQLADDQGSSEVDI HMEKAASKANI VKSFHHEESMEELF
Db 238 VIHLHQAQIHQGKHVRISRSLE	Qy 86 PGRGPRVVPHEXMLSIXRTYSIAEKLGINASFFQSSKSANTITSF-VDRGLDDLS 139
Db 218Ov 281 FTRSORKNLFAEMREOLGSAFA	Best Local Similarity 30.1%; Pred. No. 1.7e-25; Matches 120; Conservative 68; Mismatches 117; Indels 94; Gaps 16;
Qy 221 LRHQPWKQLCLELRAAWGELDA	Query Match 19.0%; Score 464; DB 2; Length 398;
Qy 171 -QAPSAPWGPPAGPLHVQLFPC : : : Db 166 VEEPSAAWERGFHRINIYEV	C; Superfamily: inhibin C; Keywords: glycoprotein F; 285-398/Product: bone morphogenetic protein 2II #status predicted <mat> F: 137, 202, 237, 340/Rinding site: carbobbotrate /ben/ /complent) #status predicted</mat>
Oy 118 FQSSKS-ANTITSF-VDRGLDI : Db 108 PERSASRANTVRSFHHEEHLES	A; Molecule type: mRNA A; Residues: 1-398 <nis> A; Cross references: GB: X63425; NID: 964583; PIDN: CAA45019.1; PID: 964584</nis>
QY 62 REGQEPQPRPQDEPRAQQPRAC : : 05 MFGLRRRPQPSKS	N. M.
QY 7 LLSAVFLISFLWDLFGFQQASI Db 7 MLWVILLCQVLLGGTNHASI	C.Species: Xenopus laevis (African clawed frog) C.Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Jul-1999 C.Accession: JH0688
Query Match 18.5%, Best Local Similarity 28.8%, Matches 138; Conservative	
A; closs references. Embl. A; close to the control of the control	Qy 414 STPPSCCVPTKLTPISILYIDAGNNVVYKQYEDMVVESCGCR 455 : : : :
A.Steatus: preliminary; translat A.Status: preliminary; translat A.Molecule type: mRNA A.Residues: 1-405 <fra></fra>	QY 354 CSKKPLHVNPKELGWDDWIIAPLEYEAYHCEGVCDFPLRSHLEPTNHAIIQTLMNSMDPG 413
A; Title: Bone morphogenetic pro A; Reference number: 150607; MUI	
R; Francis 1,0000 M. Richardson, M. Perelonment 100 000-218 1004	296 OLGSAPAAGDGAGAGGWDDDDGGADDAPAWGGAGAGGAGGAGGAGGAGGAGGAGGADAAGAGGAGGAGGA
C;Species: Gallus gallus (chick C;Date: 13-Sep-1996 #sequence_r C:Accession: 150608	QY 241 DAGEAEARARGPQQPPPDDLRSLGFGRRVRPPQERALLVVFTRSQRKNLFABMRE 295 Db 236 DNDKNVPKKHYRISRSLTPDKDNMPOIRPLLVYFSHD 272
bone morphogenetic protein 4 -	

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oteins and a signalling pathway that controls patternin ID:94163974; PMID:8119128
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                      ken)
revision 13-Sep-1996 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                              5; NID:g472929; PIDN:CAA53514.1; PID:g472930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ODL---SHIPLRRQKYLFDVSMLSDKEELVGAELRLFR-- 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PCLSPL-----LLDARTLDPQGAPPAGWEVFDVWQG 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DAGEAEARARGPQQPPPDDLRSLGFGRRVRPPQERALLVV 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AQEPPGRGPRVVPHEYMLSIYRTYSIAEK ---- LGINASF 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        :: | | | :::|::| : | | : |||||:|
ESVPGPSEAP--RIREVENLSSVPDNEVISSEELKLYREQ 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 %; Score 453; DB 2; Length 405;
%; Pred. No. 1e-24;
69; Mismatches 162; Indels 110; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --SPAVIRWTKDKOP------NHGLVIE 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EAAGPGAGAEGSWPPPSGAPDARPWLPS---PGRRRRTA 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LPQGHG----GDW-----AQLRPLLVIFGHDGRGHALIR 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KPLHVNFKELGWDDWIIAPLEYEAYHCEGVCDFPLRSHLE 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SISSSCSSAELGSTKGM----RSRKEGKMQRAPRDSDAG 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |: :: :| :| :| SLIPETGRKKVAELQGQAGSGRRSAQSHELLRGFETTLLQ 64
                                                                                     .K.; Brickell, P.M.; Tickle,
                                                                                                                                                                                               ted from GB/EMBL/DDBJ
chicken
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recursor - human genetic protein 2B

sste, A.J.; Mitsock, L.M.; Whitters, M.J.; Kriz, R.W.; revision 03-Aug-1995 #text_change 18-Jun-1999

one formation: molecular clones and activities ID:89072730; PMID:3201241

NID:g179503; PIDN:AAA51835.1; PID:g179504 OMIM:112262

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peland, N.G.; Jenkins, N.A.

Genomics 6, 505-520, 1990
A;Title: Chromosomal localization of seven members of the murine TGF-beta superfamily
A;Reference number: A34201; MUID:90228966; PMID:1970330
A;Accession: B34201
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual
A;Molecule type: mRNA
A;Residues: 253-420 <DIZ>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C,Accession: S37073
R;Feng, J.Q.; Chen, D.; Feng, M.; Harris, M.A.; Mundy, G.R.; Harris, S.E.
submitted to the EMBL Data Library, September 1993
A;Description: cDNA sequence of fetal rat calvarial osteoblast bone morphogenetic pro
A;Reference number: S37073
                                                                                                                                                                                                                                                                                                                                                                                                         19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Rattus norvegicus (Norway rat)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           118 FQSSKS-ANTITSFVDRGLDDLSHTPLRRQ----KYLFDVSMLSDKEELVGAELRLFR-- 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---RRRRTAFASRHGKRHGKKSRLRCSKKPLHVNFKELGWDDWIIAPLEYEAYHCEGVCD 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  295 HILTRRRAKRSPKHHPQRSRKKNKNCRRHSLYVDFSDVGWNDWIVAPPGYQAFYCHGDCP 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EGQEPQPRPQDEPRAQQPRAQEPPGRGPRVVPHEYMLSIYRTYSIAEK-----LGINASF 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DVWQGLRHQPWKQLCLELRAAWGELDAGEAEARARGPQQPPPPDLRSLGFGRRVRPPQER 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:Z25868; NID:g397950; PIDN:CAA81088.1; PID:g397951
C;Superfamily: inhibin
                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PERPASRANTVRSFHHE--EHLENIPGTSESSAFRFLFRLSSIPENEVISSAELRLFREQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     248 AIEVTHLHOTRTHQGQHVRISRSLPQGSGDWA------QLRPLLVTFGHDGRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   178 VDQGPDWEQGFHRINIYEVMKPPAEMVPGH-----LITRLLDTRLVHHN---VTRWETF
                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 LLSAVFLISFLWDLPGFQQASISSSCSSAELGSTKG-MRSRKEGKMQRAPRDSDA---GR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --PPAG--PLHVQLFPCLSPLLLDARTLDPQGAPPAGWEVF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   276 ALLVVFTRSQRKNLFAEMREQLGSAEAAGPGAGAEGSWPPPSGAPDARPWLPSPGR----
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                                                                                                                                                                                                                                                                                                                                                                                                         Indels 123;
                                                                                                                                                                                                                                                                                                                                                    Length 420;
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                                                                                                                                                                                                                                                                                                                                                    ; Score 436.5; DB 2;
; Pred. No. 1.6e-23;
62; Mismatches 163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 434; DB 2;
Pred. No. 2.2e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   bone morphogenetic protein 2 - rat
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30.28;
                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 28.5%
Matches 139; Conservative
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Best Local Similarity
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A; Residues: 1-393 <FEN>
                                                                                                                                                                                                                                             A;Gene: BMP-4
A;Introns: 11/1; 137/1
C;Superfamily: inhibin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             171 --QAPSAPWG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       449 VESCGCR 455
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A; Status: preliminary
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                                                                                                                                                                                                                          C; Genetics
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S37073
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C; Species: Mus musculus (house mouse)
C; Accession: 149541; S29523; B34201
R; Feng, J.Q.; Chen, D.; Cooney, A.J.; Tsai, M.; Harris, M.A.; Tsai, S.Y.; Feng, M.; Munc
A; Title: The mouse bone morphogenetic protein-4(BMP4) gene: Analysis of promoter utiliza
A; Reference number: 149541; MUID:96081880; PMID:7499338
A; Reference number: 149541; MUID:9994733; PIDN:AAC37698.1; PID:9994734
A; Residues: 1-420 < RES>
A; Cross-references: GB:L47480; NID:9994733; PIDN:AAC37698.1; PID:9994734
B; Dickinson, M.E.; van der Meer-de Jong, R.; Hogen, B.L.M.
Submitted to the EMBL Data Library, December 1990
A; December 1990
A; Peference number: S29523
A; Reference number: S29523
A; Reference number: S29523
A; Residues: 13-420 < ODIC>
A; Residues: Dickinson, M.E.; Kobrin, M.S.; Silan, C.M.; Kingsley, D.M.; Justice, M.J.; Miller, D.A
          C;Superfamily: inhibin
C;Superfamily: inhibin
E;Reywords: bone; glycoprotein
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-292/Domain: propeptide #status predicted <PRO>
F;20-292/Domain: propeptide #status predicted <PRO>
F;203-408/Product: bone morphogenetic protein 4 #status predicted <PRO>
F;143,208,350,365/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                  19;
                                                                                                                                                                                                                                                                                                                                                                                                 EGQEPQPRPQDEPRAQQPRAQEPPGRGPRVVPHEYMLSIYRTYSIAEK-----LGINAS 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FFQSSKSANTITSF-VDRGLDDLSHTPLRRQ-KYLFDVSMLSDKEELVGAELRLFRQAPS 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----SPAVLR---WIREKOPNYGLAIEVTH 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RRTAFASRHGKRHGKKSRLRCSKKPLHVNFKELGWDDWIIAPLEYEAYHCEGVCDFPLRS 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 LLSAVFLISFLWDLPGFQQASISSSCSSAELGSTKG-MRSRKEGKMQRAPRDSDA---GR 62
                                                                                                                                                                                                                                                                                                                                                                                                                           APWGP--PAGPLHVQLFPCLSP--------LLLDARTLDPQGAPPAGWEVFDVWQGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 165 VDQGPDWERGFHRINIYEVMKPPAEVVPGHLITRLLDTRLVHHN---VTRWETFDV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RHQPWKQLCLELRAAWGELDAGEAEARARGPQQPPPPDLRSLGFGRRVRPPQERALLVVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          282 TRSQRKNLFAEMREQLGSAEAAGPGAGAEGSWPPPSGAPDARPWLPSPGR------RR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LHQTRTHQGQHVRISRSLPQGS-----GNW-----AQLRPLLVTFGHDGRGHALTRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HLEPTNHAIIQTLMNSMDPGSTPPSCCVPTKLTPISILYIDAGNNVVYKQYEDMVVESCG
                                                                                                                                                                                             Length 408;
                                                                                                                                                                                             DB 1;
                                                                                                                                                                                        18.0%; Score 441.5; DB 1;
llarity 28.0%; Pred. No. 6.8e-24;
Conservative 70; Mismatches 164;
                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 455
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                                                                                                                                                                                                                     Local Simmes 135;
                                                                                                                                                                                           Query Match
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Matches
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Mon Nov 25 09:19:08 2002

	QY 341 RHGKRHGKKSRLRCSKKPLHVNF
-TPLRRQKYLFDVSMLSDKEELVGAELRLFRQAPSAPWGPPAGPLHVQLFPCLSFL 195 ::: ::	
LLDARTLDPQGAPPAGWEVFDVWQGLRHQPWKQLCLELRAAWGELDAGEARA 249	401
RGPQQPPPDLRSLGFGRRVRPPQERALLVVFTRSQRKNLFAEMREQLGSAEAAGPGAGA 309	Db 355 AIVQTLVNSVN-SSIPKACCVPT RESULT 14
250	BMHU2 BMHU2 Bone morphogenetic protein 2 prec N.Alternate names: bone morphogen C;Species: Homo sapiens (man)
310 EGSWPPPSGAPDARPWLPSPGRRRRRTAFASRHGKRSRLRCSKKP 358 C	C,Date: 16-Sep-1992 #sequence C,Accession: B37278 R;Wozney, J.M.; Rosen, V.; Ce Science 242, 1528-1534, 1988
359 LHVNFKELGWDDWIIAPLEYEAYHCEGVCDFPLRSHLEPTNHAIIQTLMNSMDPGSTPPS 418	A;Title: Novel regulators of A;Reference number: A37278; M A;Accession: B37278 A;Molecule type: mRNA
419 CCVPTKLTPISILYIDAGNNVVYKQYEDMVVESCGCR 455 A	A; Residues: 1-396 <w02> A; Cross-references: GB:M22489 R; Eshida: N:; Tsujimoto, M:; J: Biochem: 115, 279-285, 199</w02>
RESULT 13 S18343 bone morphogenetic protein 4 - rat bone morphogenetic protein 4 - rat c:Species: Rattus norvegicus (Norway rat) R:Chan, D:Species: Rattus norvegicus (Norway rat) R:Chan, D:Feng, M.; Harris, M.A.; Mundy, G.R.; Harris, S.E. B:Choing and sequence of bone morphogenetic protein 4 cDNA from fetal rat calvar A; Reference number: S18843; MUID:93385158; PMID:8373807	A; Accession: PC2178; MUID: A; Accession: PC2178; MUID: A; Molecule type: protein A; Molecule type: protein A; Experimental source: cell line R; Rathore, S; Hammerstone, K, M; Protein Sci 4 (Suppl.2), 443S, 19 A; Title: N-terminal isoforms of A; Reference number: A56729 A; Contents: annotation A; Noclecuts: annotation C; Comment: This hormone is capabl
857	C;Genetics: A;Gene: GDB:BMP2; BMP2A A;Cross-references: GDB:1252C A;Map position: 20p12-20p12 C;Complex: homodimer, disulfi
ps 19;	C; Superfamily: inhibin C; Keywords: bone; dimer; glyc F;1-23/Domain: signal sequenc F;24-265/Domain: propeptide F;266-396/Product: bone morph
20 LPGFQQASISSSCSSAELGSTKGMRSRKEGKMQRAPRDSDAGREGQEPQPRPQDEPRA 77 F	F;283-396/Product: bone morph F;135,163,164,200/Binding sit F;283/Modified site: pyrolid
128	Query Match 17.6%; Best Local Similarity 29.2%;
129 SFVDRGLDDLSHTPLRRQKYLFDVSMLSDKEELVGAELRLFRQAPSAPWG 178	Matches 49
179PPAGPLHVQLFPCLSPLLLDARTLDPQGAPPAGWEVFDVWQGLRHQPWK 227 179	23 GLVPELGRRK 101 IYRTYSIAEK : :
228 QLCLELRAAWGELDAGEARARGPQOPPPPDLRSLGFGRRVRPPOERALLVVFTRSQRK 287	Db 82 LYRRHSGQPGSPAPDHRL Qy 153 SMLSDKEELVGAELRLFRQAPSA : : : : :

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#status proglutamic acid
atus predicted <SIG>
atus predicted <PRO>
enetic protein 2, long form #status predicted <WATL>
enetic protein 2 #status predicted <WATL>
enetic protein 2 #status predicted <WATL>
carboxyliate (Asn) (covalent) #status predicted
e carboxylia caid (Gln) (in mature form) #status exper
e (Asn) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NID:g179501; PIDN:AAA51834.1; PID:g179502
naya, T.; Shimamura, A.; Tsuruoka, N.; Kodama, S.; Kat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      erization of human bone morphogenetic protein-2 in sil
D:94266754; PMID:8206877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              recombinant human bone morphogenetic protein (rhBMP-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ends of mature forms; dimers with long form chains have ble of inducing bone formation at ectopic morphologica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ste, A.J.; Mitsock, L.M.; Whitters, M.J.; Kriz, R.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ne formation: molecular clones and activities D:89072730; PMID:3201241
                                                                                                                                                                                                                                                                                                                                                                                                                          evision 03-Aug-1995 #text_change 18-Jun-1999
                                                                      Score 431.5; DB 1; Length 396;
Pred. No. 3.4e-23;
67; Mismatches 139; Indels 109; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PQDEPRAQQP-----RAQEPPGRGPRVVPHEYMLS 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FFQSSKSANTITSF-VDRGLDDLSHTPLR-RQKYLFDV 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APWGPPAGPLH-VQLFPCLSPL------LLDART 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PSDEVLSEFELRLLSMFGLKQRPTPSRDAVVP-PYMLD 81
                                                                                                                                                                           PIKLTPISILYIDAGNNVVYKQYEDMVVESCGCR 455
                                                                                                                                                                                                  e BoMo-15AIIc
.; Dansereau, S.; Porter, T.J.
1995
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enetic protein 2A; rhBMP2
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C;Species: Strongylocentrotus purpuratus (purple urchin)
C;Species: Strongylocentrotus purpuratus (purple urchin)
C;Accession: 552408
R;Ponce, M.R.; Micol, J.L.; Davidson, E.H.
Submitted to the EMBL Data Library, February 1995
A;Bescription: SpDVR1, a member of the transforming growth factor-beta superfamily expre
A;Reference number: 552408
A;Accession: 552408
A;Accession: S52408
A;Accession: 1404
A;Estiunary
A;Resiques: 1-461 <PON>
A;Coss-references: EMBL: 248313; NID: 9673496; PID: 9673497
C;Superfamily: inhibin
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                                                                                                                                                             370
LDPQGAPPAGWEVFDVWQGLRHQPWKQLCLELRAAWGELDAGEAEARARGPQQPPPPDLR 261
                                                                            SLGFGRRVRPPQERALLVVFTRSQRKNLFAEMREQLGSAEAAGPGAGAEGSWPPPSGAPD 321
                                                                                                                      -----SQ 259
                                                                                                                                                                                260 IRPLLVTFGHDGKGHPLHKREKRQA------KHKQRKRLKSSCKRHPLYVDFSDVGWND 312
                                                                                                                                                                                                                                      WIIAPLEYEAYHCEGVCDFPLRSHLEPTNHAIIQTLMNSMDPGSTPPSCCVPTKLTPISI 430
                                                                                                                                                                                                                                                               EGQEPQPRP-----QDEPRAQ-----QPRAQEPPGRGPRVVPHEYMLSIYRTYSIA 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EKLGINA-----SFFQSSKSANTITS----FVDRGLDDLSHTPLRRQKYLFDVS 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                154 MLSDKEELVGAELRLFRQAPSAPWGPPAGPLHVQLF-----PCLSPLLLDARTLDPQGA 207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         244 GDHGWLVFDMTSATSTW---RSYPGANVGLQLRVE--SLQGLNID-------PTDAG 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  262 SLGFGRRVRPPQERALLVVFTRSQ------RKNLFAEMREQLGSAEAAGPGAGAEGS 312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | : :||| | : ||
75 LGLQHRPRPPSLRGGQNQFCAQFTEWSYXRTLNIDEQSGHPSETEPQPGGLASNAIYNSP 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19 LILSLFFGPGLSWDVFYSGDEDQLSLARERRAANYNPSPHMSTWERNEIQQ----EILNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     189 RIPQGETVISAELRVFRDA--GRQGRSLYRIDVLLLRERGSDGSRSPVYLDSTIV---GA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPPPSGAPDARPWLPSPGRRRRR----TAFASRHGKRHGKKSRLRCSKKPLHVNFKELGW
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                                   197 VN-QNA--SRWESFDVTPAVMR--W-----TAQGHANHGFVVEVAHLEEKQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels 121;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17.6%; Score 429.5; DB 2; 27.7%; Pred. No. 5.5e-23; Live 68; Mismatches 177;
                                                                                                                                                                                                                                                                                                                     LYIDAGNNVYYKQYEDMVVESCGCR 455
                                                                                                                                                                                                                                                                                                                                            ||:|
|LYLDENEKVVLKNYQDMVVEGCGCR 396
                                                                                                                  --GVSKR------HVRISRSLHQD--
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Matches 140; Conservative
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202
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Search completed: November 25, 2002, 02:58:59 Job time : 52 secs



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OM protein

Run on

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DLSHTPLRRQKYLFDVSMLSDKEELVGAELRLFRQAPSAPWGPPAGPLHVQLFPCLSPLL 196
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: TBM PC compatible
COMPUTER: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Celeste, Anthony J.
APPLICANT: Wozney, John
APPLICANT: Wolfman, Wicki A.
APPLICANT: Wolfman, Neil
APPLICANT: Wolfman, Neil
APPLICANT: Wolfman, Gerald H.
APPLICANT: Welton, Obuglas A.
TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESSE:
ADDRESSEE: GENETICS INSTITUTE, INC.
STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 71.4%; Score 1747; DB 1; I
Best Local Similarity 100.0%; Pred. No. 4.3e-141;
Matches 319; Conservative 0; Mismatches 0;
                  US-08-362-670B-28
US-08-333-576C-28
US-08-808-324-28
US-08-94-14030A-28
US-08-333-576C-30
US-08-333-576C-30
US-08-334-576C-30
US-08-334-576C-30
US-08-85-559-6
US-08-455-559-13
US-08-455-559-13
US-08-456-660-13
US-08-456-660-13
US-08-456-660-13
US-08-4660-13
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US-08-808-324-4
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; Patent No. 5658882
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                              4411
4411
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; MOLECULE TYPE: protein
US-08-362-670B-26
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STATE: Massachus
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US-08-581-529B-6
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Copyright (c) 1993 - 2002
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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   DLSHTPLRRQKYLFDVSMLSDKEELVGAELRLFRQAPSAPWGPPAGPLHVQLFPCLSPLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Celeste, Anthony J.
APPLICANT: Wozney, John
APPLICANT: Wozney, John
APPLICANT: Rosen, Vicki A.
APPLICANT: Wolfman, Neil
APPLICANT: Thomsen, Gerald H.
APPLICANT: Melton, Douglas A.
TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
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100.0%; Pred. No. 4.3e-141;
tive 0; Mismatches 0;
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87 CambridgePark Drive
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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NAME: Lazar, Steven R.
REGISTRATION NUMBER: 32,618
REFERENCE/DOCKET NUMBER: 5202
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 498-8260
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STREET: 8/ C....
CITY: Cambridge
CITY: Massachusetts
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MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Celeste, Anthony J.
APPLICANT: Celeste, John
APPLICANT: Rosen, Vicki A.
APPLICANT: Noifman, Neil
APPLICANT: Holfman, Neil
APPLICANT: Melton, Douglas A.
TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/333,576C
FILING DATE: No. 6027919ember 2, 1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: GENETICS INSTITUTE, INC
STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32,618
IR: 5202-B
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Patent No. 6027919
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NAME: Lazar, Steven R.
REGISTRATION NUMBER: 32,618
REFERENCE/DOCKET NUMBER: 5202
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 498-8260
TELEPHONE: 617 498-8260
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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Matches 319; Conservative
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STATE: Massachusetts
COUNTRY: USA
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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US-08-333-576C-26
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       137 DLSHTPLRRQKYLFDVSMLSDKEELVGAELRLFRQAPSAPWGPPAGPLHVQLFPCLSPLL 196
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MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: The PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/362,670B
FILING DATE: DOCEMBER 22, 1994
CLASSIFICATION: 514
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APPLICANT: WOlfman, Nell II
APPLICANT: Thomsen, Gerald H.
APPLICANT: Melton, Douglas A.
APPLICANT: Melton, Douglas A.
APPLICANT: MELTON, TENDON-INDUCING COMPOSITIONS
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1202.5; DB 1;
Pred. No. 7.7e-95;
6; Mismatches 21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 32, Application US/08362670B Patent No. 5658882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Celeste, Anthony J. APPLICANT: Wozney, John APPLICANT: Rosen, Vicki A.
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TELEPHONE: 617 498-8260
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TELEFAX: 617 876-5851
INFORMATION FOR SEQ ID NO: 32:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               437 NNVVYKQYEDMVVESCGCR 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       303 NNVVYKQYEDMVVESCGCR 321
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Best Local Similarity 83.3%;
Matches 230; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Lazar, Steven R.
REGISTRATION NUMBER: 32,6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          263 amino acids amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Cambridge
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
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US-08-362-670B-32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
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0
                                                                       183 SGAPDARPWLPSPGRRRRRTAFASRHGKRRGKKSKLRCSKKPLHVNFKELGWDDWIIAPL 242
                                                                                                                                      257 PPDLRSLGFGRRVRPPQERALLVVFTRSQRKNLFAEMREQLGSAEAAGPGAGAEGSWPPP 316
                                                                                                                                                                                                                                   SGAPDARPWLPSPGRRRRRTAFASRHGKRRRGKKSRLRCSKKPLHVNFKELGWDDWIIAPL 376
3 DLSHTPLRRQKYLFDVSMLSDKEELVGAELRLFRQAPSAPWGPPAGPLHVQLFPCLSPLL 62
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                                              197 LDARTLDPQGAPPAGWEVFDVWQGLRHQPWKQLCLELRAAWGELDAGEAEARARGPQQPP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:

LEDP: USING TYPE: Floppy disk COMPUTER: ISLOPPY disk COMPUTER: ISLOPPY disk COMPUTER: ISLOPPY disk COMPUTER: ISON PC COMPUTED: OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTIN Release #1.0, Version #1.25 CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/14030A FILING DATE: Herewith CLASSIFICATION NUMBER: US 08/164,103 FILING DATE: 07-DEC-1993 APPLICATION NUMBER: US 08/217,780 FILING DATE: 05-MAR-1994 APPLICATION NUMBER: US 08/33,576 FILING DATE: 05-NOV-1994 ATTORNEY/AGENT INFORMATION:

REGISTRATION NUMBER: 32,618 REFERENCE/DOCKET NUMBER: 5202D-PCT TELECOMMUNICATION INFORMATION: TELECOMMUNICATION: OF SECONDER CONTRACTERISTICS: FUNNEMENT 321 AMPINO acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: GENETICS INSTITUTE, INC.
APPLICANT: PRESIDENT AND FELLOWS OF HARVARD COLLEGE
TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS
CORRESPONDENCE: 35
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: GENETICS INSTITUTE, INC.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 26, Application PC/TUS9414030A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                           NNVVYKQYEDMVVESCGCR 455
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amino acid
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us-09-825-751a-20.rai

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LDAGEAEARARGPQQPPPPDLRSLGFGRRVRPPQERALLVVFTRSQRKNLFAEMREQLGS 299
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STATE: Massachusetts
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                                                                                                                                                                                                                                                                     RESULT 7
US-08-808-324-32
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PAGPLHVQLFPCLSPLLLDARTLDPQGAPPAGWEVFDVWQGLRHQPWKQLCLELRAAWGE
                   7 PAG-----PILRGSSGTQPR---PAG-KSFDVWQGLRPQPWKQLCLELRAAWGE
                                                           240 LDAGEAEARARGPQQPPPPDLRSLGFGRRVRPPQERALLVVFTRSQRKNLFAEMREQLGS
                                                                                                                         300 AEAAGPGAGAEGSWPPPSGAPDARPWLPSPGRRRRRTAFASRHGKRHGKKSRLRCSKKPL
                                                                                                                                                                                      HVNFKELGWDDWIIAPLEYEAYHCEGVCDFPLRSHLEPTNHAIIQTLMNSMDPGSTPPSC
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                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Celeste, Anthony J.
APPLICANT: Worney, John
APPLICANT: Rosen, Vicki A.
APPLICANT: Wolfman, Neil
APPLICANT: Wolfman, Neil
APPLICANT: Melton, Douglas A.
TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSE: GENETICS INSTITUTE, INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: COMPUTER: Patentin PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/333,576C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49.1%; Score 1202.5; DB 3;
.larity 83.3%; Pred. No. 7.7e-95;
Conservative 6; Mismatches 21;
                                                                                                                                                                                                                                                                     CVPTKLTPISILYIDAGNNXVYKQYEDMVVESCGCR 263
                                                                                                                                                                                                                                                   CVPTKLTPISILYIDAGNNVVYKQYEDMVVESCGCR 455
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No. 6027919ember 2, 1994
N: 435
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STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                              Sequence 32, Application US/08333576C Patent No. 6027919 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: NO. 6027919embe
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lazar, Steven R.
REGISTRATION NUMBER: 32,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 52
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 498-8260
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LENGTH: 263 amino acids
TYPE: amino acid
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230; Conserva
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US-08-333-576C-32
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300 AEAAGPGAGAEGSWPPPSGAPDARPWLPSPGRRRRRTAFASRHGKRHGKKSRLRCSKKPL 359
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                                                                                                                                                 HVNFKELGWDDWIIAPLEYEAYHCEGVCDFPLRSHLEPTNHAIIQTLMNSMDPGSTPPSC
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                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Celeste, Anthony J.
APPLICANT: Wozney, John
APPLICANT: Wozney, John
APPLICANT: Wolfman, Weil
APPLICANT: Wolfman, Neil
APPLICANT: Thomsen, Gerald H.
APPLICANT: Thomsen, Gerald H.
APPLICANT: Thomsen, Tendon-Inducing ComPositions
ITLLE OF INVENTION: TENDON-INDUCING COMPOSITIONS
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/808,324
FILING DATE: Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1202.5; DB Pred. No. 7.7e-95; 6; Mismatches 21
                                                                                                                                                                                                                                      CVPTKLTPISILYIDAGNNVVYKQYEDMVVESCGCR 455
                                                                                                                                                                                                                                                            E: GENETICS INSTITUTE,
87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                       Sequence 32, Application US/08808324 Patent No. 6284872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32,618
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TELEPHONE: 617 498-8260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: Herewith
CLASSIFICATION: 514
ATORNEY/AGENT INFORMATION:
NAME: LAZAT, Steven R
REGISSTRATION NUMBER: 32,61'
REFRENCE/DOCKET NUMBER: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49.18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best_Local Similarity 83.3
Matches 230; Conservative
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168 HVNFKELGWDDWIIAPLEYEAYHCEGYCDFPLRSHLEPTNHAIIQIIMNSMDFGSTPPSC 227
      112 AEA----AGAEGSCPAPSGSPDTGSWLPSPGRRRRTAFASRHGKRRHGKKSRLRCSRKPL 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----PRAQEPPGRGPRVVPHEYMLSIYRTYSIAEKLGINASFFQ 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     360 HVNFKELGWDDWIIAPLEYEAYHCEGVCDFPLRSHLEPTNHAIIQTLMNSMDPGSTPPSC
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                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: H tten, Gertrud
APPLICANT: Neidhardt, Helge
APPLICANT: Paulista, Michael
TITLE OF INVENTION: NEW GROWTH/DIFFERENTIATING FACTOR OF
TITLE OF INVENTION: THE TGF- FAMILY
NUMBER OF SEQUENCES: 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Nikaido, Marmelstein, Murray & Oram LLP 655 Fifteenth Street N.W. Suite 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/288,508C
FILING DATE: 10-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
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44.7%; Pred. No. 4.6e-71;
iive 64; Mismatches 98
                                                                                                                         420 CVPTKLTPISILYIDAGNNVVYKQYEDMVVESCGCR 455
                                                                                                                                                228 CVPTKLTPISILYIDAGNNXVYKQYEDMVVESCGCR 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 10-AUG-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 43 26 829.3
FILING DATE: 10-AUG-1993
FILING DATE: 10-AUG-1993
FILING DATE: 25-MAY-1994
FILING DATE: 25-MAY-1994
FILING DATE: 09-JUN-1994
APPLICATION NUMBER: DE P 44 20 157.5
FILING DATE: 09-JUN-1994
ATTONNEY/AGENT INFORMATION:
NAME: JAHNS, KTISTIN M.
REGISTRATION NUMBER: P-41,092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: P564-4019
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)638-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                               Sequence 2, Application US/08288508C Patent No. 5994094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (202)638-4810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 44.7'
Matches 209; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: U.S.A.
ZIP: 20005-5701
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Washington
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US-08-288-508C-2
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                                                                            180 PAGPLHVQLFPCLSPLLLDARTLDPQGAPPAGWEVFDVWQGLRHQPWKQLCLELRAAWGE 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              240 LDAGEAEARARGPQQPPPPDLRSLGFGRRVRPPQERALLVVFTRSQRKNLFAEMREQLGS 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   300 AEAAGPGAGAEGSWPPPSGAPDARPWLPSPGRRRRRTAFASRHGKRHGKKSRLRCSKKPL 359
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Length 263;
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                                                                                                                                                                                                                                                                                                                                   APPLICANT: GENETICS INSTITUTE, INC.
APPLICANT: PRESIDENT AND FELLOWS OF HARVARD COLLEGE
TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSE: GENETICS INSTITUTE, INC.
STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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Pred. No. 7.7e-95;
                                                                                                                                                          420 CVPTKLTPISILYIDAGNNVVYKQYEDMVVESCGCR 455
                                                                                                                                                                                 228 CVPTKLTPISILYIDAGNNXVYKQYEDMVVESCGCR 263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/164,103
FILING DATE: 07-DEC-1993
APPLICATION NUMBER: US 08/217,780
FILING DATE: 25-MAR-1994
APPLICATION NUMBER: US 08/33,576
FILING DATE: 02-NOV-1994
ATTORNEY/AGENT INFORMATION:
RAGISTRATION NUMBER: 32,618
REFERENCE/DOCKET NUMBER: 5202D-PCT
TELECHONE: 617 498 8260
TELECHONE: 617 876-5811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: PCT/US94/14030A FILING DATE: Herewith
                                                                                                                                                                                                                                                                                              Sequence 32, Application PC/TUS9414030A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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83.3%;
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amino acid
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Best Local Similarity 83.3
Matches 230; Conservative
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MEDIUM TYPE: Floppy
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us-09-825-751a-20.rai

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ELRLFRQAP---SAPWGPPAGPL-HVQLFPCLS----PLLLDARTLDPQGAPPAGWEVFD 216
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                                                                                                                                                                                                                                                                                                                                                                                                                    ----RAOEP-----PGRGPRVVPHEYMLSIYRT
                                                                                                                              105 YSIAEKLGINASFFQSSKSANTITSFVDRGLDDLSHTPLRRQKYLFDVSMLSDKEELVGA
                                                                                                                                                                                                                                                                                                                                  ALLVVFTRSQRKNL-FAEMREQLGSAEAAGPGAGAEGSWPPPSGAPDARPWLPSPGRRRR
PGFQQASISSSCSSAELGSTKGMRSRKEGKMQRAPRDSDAGREGQEPQPRPQDE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Lee, Se-Jin
APPLICANT: Huynh, Thanh
TILLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-5
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEE: Fish & Richardson, P.C.
: 4225 Executive Square, Suite 1400
La Jolla
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APPLICATION NUMBER: 08/455,559
FILING DATE: 31-MAY-1995
APPLICATION NUMBER: 08/003,144
FILING DATE: 12-TAN-1993
ATTORNEY AGENT INFORMATION:
NAME: Lisa A. Haile, Ph.D.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/0:
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 11
US-09-145-060-10
'Sequence 10, Application US/09145060
'Patent No. 6245896
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619/678-5099
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MEDIUM TYPE: Diskett
                                                                ----PRAOOP----
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TELEFAX: 6
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                                                                                                                                                                                                                347
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             SSKSANTITSFVDRGLDDLSHTPLRRQKYLFDVSMLSDKEELVGAELRLFRQAPS----
                               253 AAPGGGRAAQL--KLSSCPSGRQPASLLDVRSV--PGLDGSGWEVFDIWKLFRNFKNSAQ
                                                                                                                                                                 L-FAEMREQLGSAEAAGPGAGAEGSWPPPSGAPDARPWLPSPGRRRRTAFASRHGKRHG
                                                                              -APWGPPAGPLHVQLFPCLS----PLLLDARTLDPQGAPPAGWEVFDVWQGLRH-QPWKQ
                                                                                                                                                                                                                                                                                KKSRLRCSKKPLHVNFKELGWDDWIIAPLEYEAYHCEGVCDFPLRSHLEPTNHAIIQTLM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: LEE, SE-JIN
APPLICANT: HUXNH, THANH
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-5
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: SPENSLEY HORN JUBAS & LUBIT2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37.6%; Score 919.5; DB 1;
43.5%; Pred. No. 2.2e-70;
Live 74; Mismatches 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: SPENSLEY HORN JUBAS & LUBITZ
STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
CITY: LOS ANGELES
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CANALATION DATE:

APPLICATION NUMBER: US/08/455,559
FILING DATE: 31-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/003,144
FILING DATE: 12-JAN-1993
ATTONNEY, AGENT INFORMATION:
NAME: WETHERELL, JR. PH.D., JOHN R. REGISTRATION NUMBER: 31,678
REGISTRATION NUMBER: DP. TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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LENGTH: 495 amino acids
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Best Local Similarity 43.5
Matches 209; Conservative
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TOPOLOGY: Linear
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MEDIUM TYPE: Floppy
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105 YSIAEKLGINASFFQSSKSANTITSFVDRGLDDLSHTPLRRQKYLFDVSMLSDKEELVGA 164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     || :|| |:::::| | |:: : | | :|
334 ALFLVFGRTKKRDLFFNEIKARSGQDDKT-------VYEYLFSQ-RRKR
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                                                                                                                                                                                                                                                                                                                                                                                           Length 495;
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APPLICANT: NEIDHARDT, HELGE
APPLICANT: BECHTOLD, ROLF
APPLICANT: BECHTOLD, ROLF
TITLE OF INVENTION: GROWTH/DIFFERENTIATION FACTORS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MURRAY & ORAM
W., G STREET LOBBY,
                                                                                                                                                                                                                                                                                                                                                                       Score 919.5; DB 5;
Pred. No. 2.2e-70;
                                             NAME: WETHERELL, JR. PH.D., JOHN R. REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: FD3256 CIP OF PD2280
                                                                                                                                                                                                                                                                                                                                                                         37.6%; Scor. 43.5%; Pred. No. 2.. 43.5%; Pred. No. 2.. 74; Mismatches "... 74; Mismatches "... PREDS.
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655 FIFTEENTH STREET, N.
SUITE 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3, Application US/08289222E Patent No. 6120760
                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: 619/455-5100
                                                                                                                                                                 TELEFAX: 619-455-5110
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 495 amino acids
                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                        TOPOLOGY: linear

MOLECULE TYPE: protein

PCT-US94-00657-10
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ADDRESSEE: NIKAIDO, 1
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                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                       TYPE: amino acid
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US-08-289-222E-3
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STREET:
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                                                                                                                                                                                                                                                                    91;
                                                                                                                                                                                                                    Length 495;
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GENERAL INPORMATION:
APPLICANT: SB-JIN LEE
APPLICANT: HUYNH, THANH
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-5
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                  37 6%; Score . 2.2e-...
43.5%; Pred. No. 2.2e-...
***A 74; Mismatches 107;
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PatentIn Release #1.0, Version #1.25
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STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
CITY: LOS ANGELES
STATE: CALIFORNIA
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                                                                                                                                                                                                                                                                                                                                                                                                               ----PRAQOP-----
                                             495 amino acids
                                                                                                                                                                                                                                                                  Conservative
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INFORMATION FOR SEQ ID NO:
                                                                                                          ; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-09-145-060-10
                      SEQUENCE CHARACTERISTICS
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FILING DATE: 1/12/9
                                                                      amino acid
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                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                           Best Local Sim
Matches 209;
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Sequence 3, Application US/09054526B Patent No. 6197550 GENERAL INFORMATION:
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437 NNVVYKQYEDMVVESCGCR 455
                   383 NNVVYKQYEDMVVESCGCR 401
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INFORMATION FOR SEQ ID NO: 3:
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Best Local Similarity 46.0
Matches 202; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                149 LFDVSMLSDKEELVGAELRLFRQAPS-----APWGPPAGPLHVQLFPCLS----PLLLD 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    199 ARTLIDPQGAPPAGWEVFDVWQGLRH-QPWKQLCLELRAAWGELDAGEAEARARGPQQPPP 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 258 PDLRSLGFGRRVRPPQERALLVVFTRSQRKNL-FAEMREQLGSAEAAGPGAGAEGSWPPP 316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 401;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NOBER: US/08/289,222E
FILING DATE: 25-AUG-1999
CLASSIFICATION: 424
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Best Local Similarity 46.0%; Pred. No. 2.4e-70;
Matches 202; Conservative 59; Mismatches 87
                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/289,222
FILING DATE: 12-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 44 23 190.3
FILING DATE: 07-JUL-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: EPO 92102324.8
FILING DATE: 12-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/00350
                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: PCT/EP93/00350 FILING DATE: 12-FEB-1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: KITTS, MONICA CHIN
REGISTRATION NUMBER: 36,105
REFERENCE/DOCKET NUMBER: P564-9021
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/638-5000
                                                                                                           COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 401 amino acids TYPE: amino acid STRANDEDNESS: single
                                                                                           Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      202/638-500
202/638-4810
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MOLECULE TYPE: protein
                                                                        COMPUTER READABLE FORM:
WASHINGTON
                                 COUNTRY: USA
ZIP: 20005-5701
                                                                                           MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-289-222E-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                   ADDRESSEE: NIKAIDO, MARMELSTEIN, MURRAY & ORAM LLP
STREET: 655 FIFTEENTH STREET, N. W., G STREET LOBBY,
STREET: SUITE 330
                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 2005-5701
COMPUTER READBLE FORM:
MEDTIN TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATE: 03-APR-1998
FILING DATE: 03-APR-1998
APPLICANT: H TTEN, GERTRUD
APPLICANT: NEIDHARDT, HELGE
APPLICANT: BECHTOLD, ROLF
APPLICANT: DOHL, JENS
TITLE OF INVENTION: DNA SEQUENCES ENCODING NOVEL
TITLE OF INVENTION: GROWTH/DIFFERENTATION FACTORS
NUMBER OF SEQUENCES: 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Score 917.5; DB 4;
; Pred. No. 2.4e-70;
59; Mismatches 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 08/289,222
FILING DATE: 12-AUG-1994
PRIOR APPLICATION DATE:
APPLICATION NUMBER: DE P 44 23 190.3
FILING DATE: 01-7UL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EPO 92102324.8
FILING DATE: 12-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: PCT/FE93/00350
FILING DATE: 12-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: KITTS, MONICA CHIN
RGGISTRATION NUMBER: 36,105
REFERENCE/DOCKET NUMBER: P564-8005
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LFDVSMLSDKEELVGAELRLFRQAPS-----APWGPPAGPLHVQLFPCLS----PLLLD 198
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                                                                     ARTLDPQGAPPAGWEVFDVWQGLRH-QPWKQLCLELRAAWGELDAGEAEARARGPQQPPP
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                                                                                         78; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Celeste, Anthony J.
APPLICANT: Wozney, John
APPLICANT: Wolfman, Vicki A.
APPLICANT: Wolfman, Neil
APPLICANT: Wolfman, Gerald H.
APPLICANT: Thomsen, Gerald H.
APPLICANT: Thomsen, Thomsen, Gerald H.
APPLICANT: Thomsen, Tendon Tendon Inductive Sequences:
TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/362,670B
FILING DATE: December 22, 1994
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 31.3%; Score 765; DB 1; Best Local Similarity 51.2%; Pred. No. 2.3e-57; Matches 172; Conservative 36; Mismatches 78,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: GENETICS INSTITUTE, INC
STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 34, Application US/08362670B Patent No. 5658882
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NAME: Lazar, Steven R.
REGISTRATION NUMBER: 32,618
REFERENCE/DOCKET NUMBER: 5202
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617,498-8260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 34: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                            NNVVYKQYEDMVVESCGCR 455
                                                                                                                                                                                                                                                                                                                                                                               388 amino acids
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Massachusetts
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US-08-362-670B-34
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STATE:
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PPPDLRSLGF---GRRVRPPQERALLVVFTRSQRK-NLFAEMREQ---LGSAEAAGPGAG 308
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                                                    201 TLDPQGAPPAGWEVFDVWQGLRH-----QPWKQLCLELRAAWGELDAGEAEARARGPQQP 255
                                                                                                                                       237
                                                                                                                                                                   309 AEGSWPPPSGAPDARPWLPSPGRRRRTAFASRH-----GKRHGKKSRLRCSKKPL 359
                                                                                                                                                                                                                                    360 HVNFKELGWDDWIIAPLEYEAYHCEGVCDFPLRSHLEPTNHAIIQTLMNSMDPGSTPPSC
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Search completed: November 25, 2002, 02:59:49 Job time : 37 secs

Sequence 12, Appl Sequence 8, Appli Sequence 14, Appl Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 10, Appli

Appli

Sequence 4, Sequence 2, Sequence 6, Sequence 32, Sequence 31, Sequence 28,

Sequence 24,

Sequence

Appli Appli Appli Appli Appli Appli Appli

Sequence 2, 1 Sequence 2, 2 Sequence 13, 2 Sequence 2, 8 Sequence 2, 8 Sequence 15, 8

Appli Appl Appl

> Sequence 37, Sequence 15,

Sequence 1,

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GENERAL INFORMATION:
APPLICANT: Luyten, Frank P.
APPLICANT: MOSs, Jr., Malcolm
APPLICANT: Chang, Steven Chao-Huan
TITLE OF INVENTION: CARTILAGE-DERIVED MORPHOGENETIC
TITLE OF INVENTION: PROTEINS
         US-09-952-360-2
US-09-813-398-24
US-09-813-398-24
US-09-784-911-2
US-09-813-398-31
US-09-813-398-31
US-09-813-398-31
US-09-813-398-31
US-09-813-398-28
US-09-813-398-28
US-09-813-398-28
US-09-813-398-28
US-09-813-398-28
US-09-822-186-2
US-08-922-186-2
US-08-937-755-2
US-09-982-543A-10
US-09-982-543A-10
US-09-982-643-10
US-09-982-182-13
US-09-982-182-13
US-09-982-182-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: Knobbe, Martens, Olson & Bear
620 Newport Center Drive, 16th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: Windows SOFTWARE: FastSEQ for Windows Version 2.0b CURRENT APPLICATION DATA:
FILING DATE:
                                                                                                                                                                                                                                                  US-09-945-182-15
US-10-084-037-1
                                                                                                                                                                                                                                                                         US-09-859-211-37
US-09-880-708-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Bartfeld, Neil S
REGISTRATION NUMBER: 39,901
REFERENCE/DOCKET NUMBER: NIH099.001APC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-235-8550
                                                                                                                                                                                                                                                                                                                                                                             Sequence 14, Application US/09730772 Patent No. US20010011131A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PARIOR APPLICATION NUMBER: 08/836,081
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 436 amino acids
TYPE: amino acid
          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Competible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 619-235-0176
STREET: 620 Newport
CITY: Newport Beach
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 92660
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US-09-730-772-14
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416.5
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 Sequence 13, Appl
Sequence 34, Appl
Sequence 2, Appli
Sequence 28, Appl
Sequence 30, Appl
Sequence 11, Appli
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Sequence 2, Appli
Sequence 4, Appli
Sequence 69, Appl
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Sequence 14, App
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Sequence 37, Appl
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Sequence 32, Appl
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                                                                                        (without alignments)
237.533 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 13,
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                                                                                                                    US-09-825-751A-20
2447
1 MDTPRVLLSAVFLISFLMDL......GNNVVXKQYEDMVVESCGCR
                                                                         November 25, 2002, 02:55:26 ; Search time 30 Seconds
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/ Cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
/ Cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
/ Cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*
/ Cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*
/ Cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*
/ Cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
/ Cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
/ Cgn2_6/ptodata/1/pubpaa/USO9_NEW_PUB.pep:*
/ Cgn2_6/ptodata/1/pubpaa/USO9_NEW_PUB.pep:*
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         GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-945-182-26
US-09-945-182-32
US-09-981-182-32
US-09-880-708-10
US-09-813-398-37
US-09-945-182-34
US-09-945-182-2
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US-09-880-708-13
US-09-068-253-2
US-09-945-182-4
                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
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US-09-735-849-14
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Maximum Match 100%
Listing first 45 summaries
                                                     OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Match Length
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Perfect score:
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Maximum DB
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TOPOLOGY:
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US-09-735-849-14
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Matches 354;
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                                                                                           Gaps
                                                                                                                     33 SSAELGSTKGMRSRKEGKMQRAPRDSDAGRE---GQEPQPRPQDEPR---AQQPRAQEPP 86
                                                                                                                                            2 ASAELGSAKGMRTRKEGRMPRAPRENATAREPLDRQEPPRPQEEPQRRPPQQPEAREPP 61
                                                                                                                                                                                                                                                                             APPAGWEVFDVWQGLRHQPWKQLCLELRAAW-GELDAGEAEARARGPQQPPPPDLRSLGF
                                                                                                                                                                                                                                                                                            GRRVRPPQERALLVVFTRSQRKNLFAEMREQLGSA-EAAGPGAGAEGSW-----PPPPS
                                                                                                                                                                                                                                                                                                                                             KYLFDVSMLSDKEELVGAELRLFRQAPSAPWGPPAGPLHVQLFPCLSPLLLDARTLDPQG
                                                                                           18;
                                                                 Length 436;
                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Luyten, Frank P.
APPLICANT: Moos, Jr., Malcolm
APPLICANT: Chang, Steven Chao-Huan
TITLE OF INVENTION: CARTILAGE-DERIVED MORPHOGENETIC
TITLE OF INVENTION: PROTEINS
                                                               73.5%; Score 1798; DB 10;
80.8%; Pred. No. 2.6e-120;
iive 18; Mismatches 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: G20 Newport Center Drive, 16th Floor
CITY: Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastESQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US/09/735,849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 14, Application US/09735849
Patent No. US20010037017A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 08/836,081 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE:
COUNTRY: U.S.A.
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
AMDIUM TYPE: Diskette
TYPE: IBM Compatible
TYPE: IBM Compatible
TYPE: TIPM COMPANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NVVYKQYEDMVVESCGCR 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION
                                                              Query Match 73.5
Best Local Similarity 80.8
Matches 354; Conservative
            TOPOLOGY: linear MOLECULE TYPE: peptide
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE
                                      US-09-730-772-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-735-849-14
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STATE:
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GRGPRVVPHEYMLSIYRTYSIAEKLGINASFFQSSKSANTITSFVDRGLDDLSHTPLRRQ 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  122 KYLFDVSTLSDKEELVGADVRLFRQAPAALAPPAAAPAALRIP-VAPAAGSAEP-GPAG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1359 YEAYHCEGVCDFPLRSHLEPINHAIIQTLMNSMDPGSTPPSCCVPTKLTPISILYIDAGN 418
                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GRGPRLVPHEYMLSIYRTYSIAEKLGINASFFQSSKSANTITSFVDRGLDDLSHTPLRRQ 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KYLFDVSMLSDKEELVGAELRLFRQAPSAPWGPPAGPLHVQLFPCLSPLLLDARTLDPQG 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              207 APPAGWEVFDVWQGLRHQPWKQLCLELRAAW-GELDAGEAEARARGPQQPPPPDLRSLGF 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GRRVRPPQERALLVVFTRSQRKNLFAEMREQLGSA-EAAGPGAGAEGSW-----PPPS 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAPDARPWLPSPGRRRRRTAFASRHGKRHGKKSRLRCSKKPLHVNFKELGWDDWIIAPLE 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           378 YEAYHCEGVCDFPLRSHLEPTNHAIIQTLMNSMDPGSTPPSCCVPTKLTPISILYIDAGN 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                       33 SSAELGSTKGMRSRKEGKMQRAPRDSDAGRE---GQEPQPRPQDEPR---AQQPRAQEPP 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18;
                                                                                                                                                                                                                                                                                                                                                                    Length 436;
                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wolfman, Neil
Thomsen, Gerald H.
Melton, Douglas A.
TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS
                                                                                                                                                                                                                                                                                                                                                                73.5%; Score 1798; DB 10;
80.8%; Pred. No. 2.6e-120;
tive 18; Mismatches 48;
                                                                                                                                                                                                                                                                                                                                                                    DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: GENETICS INSTITUTE, INC
STREET: 87 CambridgePark Drive
                                                            NIH099.001APC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 26, Application US/09945182 Patent No. US20020160494A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Celeste, Anthony J.
Bartfeld, Neil S
                                   REGISTRATION NUMBER: 39,901
REFERENCE/DOCKET NUMBER: NII
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-235-855
TELEPAX: 619-235-0176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wozney, John
Rosen, Vicki A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
ZIP: 02140
                                                                                                                                            TELEX:
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 436 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NVVYKQYEDMVVESCGCR 455
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                               : 436 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                           single
                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                               linear
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APPLICANT: Hotten, Gertrud
APPLICANT: Pohl, Jens
APPLICANT: Pohl, Jens
APPLICANT: Beckhold, Rollf
APPLICANT: Paulista, Michael
APPLICANT: Tonsicker, Klaus
TITLE OF INVENTION: USE OF MP52 OR MP121 FOR TREATING AND PREVENTING DISEASES OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      180 PAGPLHVQLFPCLSPLLLDARTLDPQGAPPAGWEVFDVWQGLRHQPWKQLCLELRAAWGE 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      240 LDAGEAEARARGPQQPPPPDLRSLGFGRRVRPPQERALLVVFTRSQRKNLFAEMREQLGS 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               300 AEAAGPGAGGAEGSWPPPSGAPDARPWLPSPGRRRRRTAFASRHGKRHGKKSRLRCSKKPL 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       360 HVNFKELGWDDWIIAPLEYEAYHCEGVCDFPLRSHLEPTNHAIIQTLMNSMDPGSTPPSC 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49.1%; Score 1202.5; DB 9; Length
83.3%; Pred. No. 2.1e-78;
.ive 6; Mismatches 21; Indels
                                                                                                                                       Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        420 CVPTKLTPISILYIDAGNNVVYKQYEDMVVESCGCR 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                228 CVPTKLTPISILYIDAGNNXVYKQYEDMVVESCGCR 263
                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/945,182
FILING DATE: 31-Aug-2001
CLASSIFICATION: <Unknown>
                                                                                                                                       SOFTWARE: Patentin Release #1.0,
                                                                                            COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 5202-D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: NERVOUS SYSTEM
FILE REFERENCE: 100564-07032
CURRENT APPLICATION NUMBER: US/08/981,490B
CURRENT FILING DATE: 1998-05-18
PRIOR APPLICATION NUMBER: PCT/EP96/03065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 32:
US-09-945-182-32
                                                                                                                                                                                                                                       NAME: Lazar, Steven R. REGISTRATION NUMBER: 32,618
                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 498-8260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/08981490B
Patent No. US20020045568A1
GENERAL INFORMATION:
                                                                           MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 263 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 617 876-5851
                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 32
                                                     COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 230; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
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US-08-981-490B-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 137 DLSHTPLRRQKYLFDVSMLSDKEELVGAELRLFRQAPSAPWGPPAGPLHVQLFPCLSPLL 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LDARTLDPQGAPPAGWEVFDVWQGLRHQPWKQLCLELRAAWGELDAGEAEARARGPQQPP 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SGAPDARPWLPSPGRRRRRTAFASRHGKRHGKKSRLRCSKKPLHVNFKELGWDDWIIAPL 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 DLSHTPLRRQKYLFDVSMLSDKEELVGAELRLFRQAPSAPWGPPAGPLHVQLFPCLSPLL 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EYEAYHCEGVCDFPLRSHLEPTNHAIIQTLMNSMDPGSTPPSCCVPTKLTPISILYIDAG
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
RAPPLICATION NUMBER: US/09/945,182
FILING DATE: 31-Aug-2001
CLASSIFICATION: <Unknown>
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TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 5202-D
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 498-8260
TELEFAX: 617 876-5851
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE DESCRIPTION: SEQ ID NO: 26:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: GENETICS INSTITUTE, STREET: 87 CambridgePark Drive
                                                                                                                                                                   APPLICATION NUMBER: 08/808,324
FILING DATE: <URNOWN>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                 NAME: Lazar, Steven R. REGISTRATION NUMBER: 32,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 32, Application US/09945182
Patent No. US2002016049A1
GENERAL INFORMATION:
APPLICANT: Celeste, Anthony J.
Nozney, John
Rosen, Vicki A.
Wolfman, Neil
Thomsen, Gerald H.
                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 321 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
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                                                                                                                                                   PRIOR APPLICATION DATA:
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Matches 319; Conserva
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US-09-945-182-32
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APPLICATION NUMBER: 09/145,060
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                                                                                                                                                 INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 495 amino acids
                                                                                                                              TELEPHONE: 858/677-1456
TELEFAX: 619/677-1465
                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                      Matches 209; Conservative
                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                   US-09-880-708-10
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US-09-813-398-37
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                                                                                                                                                                                                                                                                                   174
                                                                                                                                                                                                                                                                                                                                      253 AAPGGGRAAQL--KLSSCPSGRQPASLLDVRSV--PGLDGSGWEVFDIWKLFRNFKNSAQ 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           347
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                                                                                                                                                                                                                                                                                                                       SSKSANTITSFVDRGLDDLSHTPLRRQKYLFDVSMLSDKEELVGAELRLFRQAPS----
                                                                                                                                                                                                                                                                                                                                                                                                                                   LCLELRAAWGELDAGEAEARARGPQOPPPDLRSLGFGRRVRPPQERALLVVFTRSQRKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                             LCLELE-AW---ERGRA------VDLRGLGFDRAARQVHEKALFLVFGRTKKRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          L-FAEMREQLGSAEAAGPGAGAEGSWPPPSGAPDARPWLPSPGRRRRRTAFASRHGKRHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KKSRLRCSKKPLHVNFKELGWDDWIIAPLEYEAYHCEGVCDFPLRSHLEPTNHAIIQTLM
                                                                                                                                                                                                                                                                                                                                                                             -APWGPPAGPLHVQLFPCLS----PLLLDARTLDPQGAPPAGWEVFDVWQGLRH-QPWKQ
                                                                                                                                                                                97;
                                                                                                                                                      Length 501;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NSMDPGSTPPSCCVPTKLTPISILYIDAGNNVVYKQYEDMVVESCGCR 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-5 NUMBER OF SEQUENCES: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 92121-2189
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ware & Freidenrich e Drive, Suite 1600
                                                                                                                                                     37.9%; Score 927.5; DB 8;
44.7%; Pred. No. 1.3e-58;
ilve 64; Mismatches 98;
                                                                                                                                                                                                           38 GSTKGMRSRKEGKMQRAPRDSDAGREGQEPQPRPQDEPRAQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/880,708
FILING DATE: 12-Jun-2001
PRIOR APPLICATION DATA:
PRIOR FILING DATE: 1996-07-12
PRIOR APPLICATION NUMBER: DE/195 25 416.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 10, Application US/09880708
Patent No. US20020165361A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Gray Cary Wa
STREET: 4365 Executive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION DATA:
                        PRIOR FILING DATE: 1995-07-12
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3.1
SEQ ID NO LENGTH: 501
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                                                                                                                                                                Best Local Similarity 44.7 Matches 209; Conservative
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STATE: CA
                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
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Patent No. US20020169292A1
GENERAL INFORMATION:
APPLICANT: Bruce D. Weintraub
APPLICANT: Mariusz W. Szkudlinski
APPLICANT: University of Maryland
APPLICANT: University of Maryland
TITLE OF INVENTION: CYSTINE KNOT GROWTH FACTOR MUTANTS
FILE REPERENCE: UOFMD.003C1
CURRENT APPLICATION NUMBER: US/09/813,398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37.6%; Score 919.5; DB 9;
43.5%; Pred. No. 4.6e-58;
iive 74; Mismatches 107;
                                                                                                    NAME: Lisa A. Haile, Ph.D.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/057002
                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
TOPOLGOY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/003,144
FILING DATE: 12-JAN-1993
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81 GOTGGLTOPKKDEPKKLPPRPGGPEPKRGHPPOTROATARTVTPKGOLPGGKAPPKAGSV 140
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es 108; Indels
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Patent No. US20010037017A1
GENERAL INFORMATION:
APPLICANT: Luylen, Frank P.
APPLICANT: Moos, Jr., Malcolm
APPLICANT: Chang, Steven Chao-Huan
TITLE OF INVENTION: CARTILAGE-DERIVED MORPHOGENETIC
TITLE OF INVENTION: PROTEINS
NUMBER OF SEQUENCES: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TPPSCCVPTKLTPISILYIDAGNNVVYKQYEDMVVESCGCR 455
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; Pred. No. 6.3e
63; Mismatches
                                                                                                                                                                                               NIH099.001APC
                           US/09/730,772
                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/836,081
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Bartfeld, Nell S
REGISTRATION NUMBER: 39,91
REFERENCE/DOCKET NUMBER: NIH099.
                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-235-8550
TELEFAX: 619-235-0176
                                                                                                                                                                                                                                                                                                13:
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44.98;
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                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: peptide
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                           APPLICATION NUMBER:
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Best Local Similarity
                                                                 CLASSIFICATION:
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Patent No. US20010011131A1
GENERAL INFORMATION:
APPLICANT: Luyten, Frank P.
APPLICANT: Moos, Jr., Malcolm
APPLICANT: Chang, Steven Chao-Huan
TITLE OF INVENTION: RATILAGE-DERIVED MORPHOGENETIC
TITLE OF INVENTION: PROTEINS
NUMBER OF SEQUENCES: 24
                                                                                                                                                                                                                                                                                          64; Mismatches 101;
                                                                                                                                                                                                                                                    37.5%; Score 918.5; DB 9; 44.3%; Pred. No. 5.5e-58;
                                                                                                                                                                                                                                                                                                                              38 GSTKGMRSRKEGKMQRAPRDSDAGREGQEPQPRPQDEPRAQQ-
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STREET: 620 Newport Center Drive, 16th Floor
CITY: Newport Beach
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FastSEQ for Windows Version 2.0b
CURRENT FILING DATE: 2001-03-20
PRIOR APPLICATION NUMBER: PCT/US99/05908
PRIOR FILING DATE: 1999-03-19
PRIOR APLICATION NUMBER: PCT/US98/19772
PRIOR FILING DATE: 1998-09-22
NUMBER OF SEQ ID NOS: 41
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 37
LENGTH: 502
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MEDIUM TYPE: Diskette
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                                                                                                                                                                                           ORGANISM: HOMO SAPIEN
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US-09-730-772-13
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                                                                                                                                                                               TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 10; Length 501;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 36.9%; Score 903.5; DB 10; Best Local Similarity 44.9%; Pred. No. 6.3e-57; Matches 207; Conservative 63; Mismatches 108;
:: Knobbe, Martens, Olson & Bear
620 Newport Center Drive, 16th Floor
                                                                                                                   COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FRASTSO for Windows Version 2.0b
CURRENT APPLICATION DATA:
FILING DATE:
                                                                                                                                                                                                                                                                ATTORNEY AGENT INFORMATION:
NAME: Bartfeld, Neil S
REGISTRATION NUMBER: 39,901
REFERENCE/DOCKET NUMBER: NIH099.001APC
TELECOMUNICATION INFORMATION:
TELEPHONE: 619-235-8550
TELEFAX: 619-235-0176
                                                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/836,081
FILING DATE:
                                                                    ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 501 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                        single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE: peptide US-09-735-849-13
            STREET: brows.r.r.ccITY: Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                           U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                         COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         201 TLDPQGAPPAGWEVFDVWQGLRH----QPWKQLCLELRAAWGELDAGEAEARARGPQQP 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        256 PPPDLRSLGF---GRRVRPPQERALLVVFTRSQRK-NLFAEMREQ---LGSAEAAGPGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      309 AEGSWPPPSGAPDARPWLPSPGRRRRTAFASRH------GKRHGKKSRLRCSKKPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 360 HVNFKELGWDDWIIAPLEYEAYHCEGVCDFPLRSHLEPTNHAIIQTLMNSMDPGSTPPSC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31.3%; Score 765; DB 9; Length 388; 51.2%; Pred. No. 3e-47; Live 36; Mismatches 78; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                          TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS NUMBER OF SEQUENCES: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CVPTKLTPISILYIDAGNNVVYKQYEDMVVESCGCR 455
                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: GENETICS INSTITUTE, INC
STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/945,182
FILING DATE: 31-Aug-2001
CLASSIFICATION: <un>

Unknown>

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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 34:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/808,324

FILING DATE: <UNKNOWN>

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Lazar, Steven R.
REGISTRATION NUMBER: 32,618
REFERENCE/DOCKET NUMBER: 52
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 498-826
TELEFAX: 617 876-5851
Sequence 34, Application US/09945182
Patent No. US20020160494A1
GENERAL INFORMATION:
APPLICANT: Celeste, Anthony J. Wozney, John
Rosen, Vicki A. Wolfman, Neil
Thomsen, Gerald H. Thomsen, Gerald H. Melton, Douglas A.
                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 388 amino acids
                                                                                                                                                                                                                                                                                                                                                STATE: Massachusetts
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SEQUENCE CHARACTERISTICS
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Matches 172; Conservative
                                                                                                                                                                                                                                                                                                                      CITY: Cambridge
                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          137 SSIPTEEFITSAELQVFREQMQDALGNNSSFHHRINIYEIIKPATANSKFPVTRLLDTRL 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        101 IYRTYSIAEKLGINAS-----FFQSSKSANTITSF-VDRGLDDLSHTPLR-RQKYLFDV 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMLSDKEELVGAELRLFRQAPSAPWGPPAGPLH-VQLFPCLSPL------LLDART 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 202 LDPQGAPPAGWEVFDVWQGLRHQPWKQLCLELRAAWGELDAGEAEARARGPQQPPPPDLR 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       262 SLGFGRRVRP-----PQERALLVVFTRSQRKNLF--AEMREQL-GSAEAAGPGAGAEGSW 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49 GKMQRAPRDSDAGREGQEPQPRPQDEPRAQQP-----RAQEPPGRGPRVVPHEYMLS 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
       251 PDAAPASCCVPARLSPISILYIDAANNVVYKQYEDMVVEACGCR 294
                                                                                                                                                                                                                                                                                                                                                                               Wolfman, Neil
Thomsen, Gerald H.
Melton, Douglas A.
INVENTION: TENDON-INDUCING COMPOSITIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25.6%; Score 627; DB 9; I
37.1%; Pred. No. 1.9e-37;
tive 54; Mismatches 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: GENETICS INSTITUTE, INC
STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/945,182
FILING DATE: 31.Aug-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 28:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 08/808,324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Lazar, Steven R.
REGISTRATION NUMBER: 32,618
REFERENCE/DOCKET NUMBER: 520
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 498-8260
TELEPHONE: 617 876-5851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                Celeste, Anthony J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                      Sequence 28, Application US/09945182 Patent No. US20020160494A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 411 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: <Unknown> ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                   Wozney, John
Rosen, Vicki A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 25.63
Best Local Similarity 37.13
Matches 164; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cambridge
                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                          RESULT 12
US-09-945-182-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-945-182-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                248 RARGPQQPPPDLRSLGF---GRRVRPPQERALLVVFTRSQRK-NLFAEMREQ---LGSA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                301 EAAGPGAGAEGSWPPPSGAPDARPWLPSPGRRRRRTAFASRH------GKRHGKKSR 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          352 LRCSKKPLHVNFKELGWDDWIIAPLEYEAYHCEGVCDFPLRSHLEPTNHAIIQTLMNSMD 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/945,182
FILING DATE: 31-A04-2001
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PGSTPPSCCVPTKLTPISILYIDAGNNVVYKQYEDMVVESCGCR 455
                                                                                                                                                                                                                                                                                                                                                                                                                                               Melton, Douglas A.
DF INVENTION: TENDON-INDUCING COMPOSITIONS
OF SEQUENCES: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    353 CVPARLSPISILYIDAANNVYKQYEDMVVEACGCR 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: GENETICS INSTITUTE, INC. STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Lazar, Steven R.
REGISTRATION NUMBER: 32,618
REFERENCE/DOCKET NUMBER: 5202-D
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 498 8260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TOPOLOGY: linear; MOLECILE TYPE: protein; SEQUENCE DESCRIPTION: SEQ ID NO: 2: US-09-945-182-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/808,324
                                                                                                                                                                                                                                                                                                                                                                            Wolfman, Neil
Thomsen, Gerald H.
                                                                                                                                                                  Sequence 2, Application US/09945182
Patent No. US20020160494A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 294 amino acids
                                                                                                                                                                                                                                                                     APPLICANT: Celeste, Anthony
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                            Wozney, John
Rosen, Vicki A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 617 876-5851 INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: TEN
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 53.29
Matches 151; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                      RESULT 11
US-09-945-182-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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                                                             402 IIQTLMNSMDPGSTPPSCCVPTKLTPISILYIDAGNNVVYKQYEDMVVESCGCR 455
                                                                                                                                    Length 119;
                                                                                                                                                                                                                                                                                                                       APPLICANT: HIROYUKI; MIKI, HIDED; KAWAI,
APPLICANT: SHINJI; KIMURA, MICHIO; MATSUMOTO,
APPLICANT: TOMOAKI; KATSUURA, MIEKO; ENOMOTO,
APPLICANT: SATOH; YUSUKE
TITLE OF INVENTION: A NOYEL PROTEIN AND
TITLE OF INVENTION: PROCESS FOR PREPARING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BIERMAN, MUSERLIAN AND LUCAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22.4%; Score 549;
                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: MAKISHIMA, FUSAO; TAKAMATSU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MICROSOFT WORD 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/945,459A
FILING DATE: 09-DEC-1997
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: PCT/JP96/01062
FILING DATE: 19-APR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP7/322403
FILING DATE: 17-NOV-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      146.1275
                                                                                                                                                                                                                                                  Sequence 1, Application US/08945459A Patent No. US20020102633A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: CHARLES A. MUSERLIAN REGISTRATION NUMBER: 19,683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (212) 661-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    600 THIRD AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 19-APR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (212) 661-8002
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AMINO ACID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: LINEAR
MOLECULE TYPE: PEPTIDE
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: FLOPPY I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             383 TO 501
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ADDRESSEE: BIERMAN,
                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
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                                                                                                                                                                                                              RESULT 14
US-08-945-459A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
US-08-945-459A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET:
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243 HVRISRSLHQDEHSWSQIRPLLVTFGHDGKGHPLHKREKRTALAGTRTAQGSGGGA---- 298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          314 PPPSGAPDARPWLPSPGRRRRTAFASRHGKRHGKKSRLRCSKKPLHVNFKELGWDDWII
                                                             APLEYEAYHCEGVCDFPLRSHLEPTNHAIIQTLMNSMDPGSTPPSCCVPTKLTPISILYI
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55.6%; Pred. No. 4.5e-37;
Live 20; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC Compatible
SEARING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                      Wolfman, Neil
Thomsen, Gerald H.
Melton, Douglas A.
TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AEGSWPPPSGAPDARPWLPS-PGRRRRRTAFASRH-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURREMY APPLICATION DATA:

APPLICATION NUMBER: US/09/945,182
FILING DATE: 31-Aug-2001
CLASSIFICATION: CURKNOWN>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Lazar, Steven R.
REGISTRATION NUMBER: 32,618
REFERENCE/DOCKET NUMBER: 5202-D
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MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 30:
US-09-945-182-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 08/808,324 FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 498-8260
TELEFAX: 617 876-5851
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Celeste, Anthony J.
                                                                                                                                                                                                                                                                                                                         Sequence 30, Application US/09945182 Patent No. US20020160494A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 240 amino acids
                                                                                                                                                                                                            Wozney, John
Rosen, Vicki A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: Massachusetts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
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                                                                                                                                                                                                                                                                                     RESULT 13
US-09-945-182-30
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Matches 130;
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                                                           339 ASRHGKRHGKKSRLRCSKKPLHVNFKELGWDDWIIAPLEYEAYHCEGVCDFPLRSHLEPT 398
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                         Gaps
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                                                                                                                                                                  63 NHAVIQTLANSMDPESTPPTCCVPTRLSPISILFIDSANNVYKQYEDMVVESCGCR 119
                       ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22.4%; Score 549; DB 9; Length 11
80.3%; Pred. No. 1.6e-32;
tive 14; Mismatches 9; Indels
Best Local Similarity 80.3%; Pred. No. 1.6e-32;
Matches 94; Conservative 14; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-5 NUMBER OF SEQUENCES: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Gray Cary Ware & Freidenrich LLP STREET: 4365 Executive Drive, Sulte 1600 CITY: San Diego STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 92121-2189
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Lisa A. Haile, Ph.D.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/057002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 858/677-1456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:

APPLICATION NUMBER: U$/09/880,708
FILING DATE: 12-Jun-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/145,060
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/003,144
FILING DATE: 12-JAN-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE DESCRIPTION: SEQ ID NO: 13: US-09-880-708-13
                                                                                                                                                                                                                                                                                      Sequence 13, Application US/09880708 Patent No. US20020165361A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 119 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 619/677-1465
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Lee, Se-Jin
                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 80.3%
Matches 94; Conservative
                                                                                                                                                                                                                                               RESULT 15
US-09-880-708-13
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Search completed: November 25, 2002, 03:00:33

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Perfect score:

Sequence:

OM protein

Scoring table:

Searched:

Minimum DB Maximum DB

Maximum

Database

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Q90yj3 brachydanio Q9pvk1 gallus gall Q9bvk1 gallus gall Q91597 kenopus lae Q9xq8 strongyloce Q013109 brachydanio Q9xyc5 canis famil P91720 drosophila Q73818 kenopus lae Q9xx5 canis famil P91720 drosophila Q93369 brachydanio Q91703 xenopus lae P8737 gallus gall Q90yd6 kenopus lae P8737 gallus gall Q90yd6 kenopus lae P8737 gallus gall Q90yd6 kenopus lae Q9x69 tripneustes P87380 brachydanio Q97390 crassostrea Q9xx69 tripneustes P87380 brachydanio Q91403 gallus gall
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076851 halocynthia
090y81 lampetra ja
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
GTOWth and differentiation factor 6.
GDF6.
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PROSITE; PS00250; TGF_BETA_1; 1.
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Best Local Similarity 58.89
Matches 270; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
   Glycoprotein
SEQUENCE 39
                    445
442
439.5
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                                                                                            Q9W753
Q9W753;
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     Q9W753
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029dgn4 xenopus lae
0294gg gallus gall
029bdw8 cercopithec
029jw9 gallus gall
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                                                                                                                      November 25, 2002, 02:50:50 ; Search time 91 Seconds (without alignments) 1030.236 Million cell updates/sec
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                    GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                             671580 segs, 206047115 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                        - protein search, using sw model
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09DGN4
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sp_rodent:*
sp_virus:*
sp_vertebrate:*
sp_unclassified:*
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2447
1 MDTPRVLLSAVFLISFLWDL.
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Gapop 10.0 , Gapext 0.5
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sp_human:*
sp_invertebrate:*
sp_mammal:*
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sp_bacteria:*
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Match Length DB
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Score

Result 8

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Query Match
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bruneau S., Rosa F.,
"Dynamo a new Zebrafish DVR member of the TGF-B superfamily is
expressed in the posterior neural tube and is up regulated by Sonic
                                     DAGRECQEPQPRPQDEPRAQQPRAQEPPGRGPRVVPHEYMLSIYRTYSIAEKLGINASFF
                                                PPAGPLHVQLFPCLSPLLLDARTLDPQGAPPAGWEVFDVWQGLR--HQPWKQLCLELRAA
                                                                                                                              152 TPLDLYNLQVTSCTSQAQLDYRTLDLRDTPSPGWQVFDVWKSLQDISQGKKQICVELKAI
                                                                                                                                                       WGELDAGEAEARARGPQOPPPPDLRSLGFGRRVRPPQERALLVVFTRSQRKNLFAEMREQ
                                                                                                                                                                  KPLHVNFKELGWDDWIIAPLEYEAYHCEGVCDFPLRSHLEPTNHAIIQTLMNSMDPGSTP
1 MDTPR--VLLSAVFLISFLWDLPGFQQASISSSCSSAELGSTKGMRSRKEGKMQRAPRDS
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                  1 MDTYRSPLPVSLLLFILLLWEVPCIQQASIPSALQPGAL----RRQRREDKVSSYSAD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DYNAMO PROTEIN.
4076E262C4481121 CRC64;
                                                                                                                                                                                                                                                                                                                                                            01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                  PSCCVPTKLTPISILYIDAGNNVVYKQYEDMVVESCGCR 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hedgehog.";
Mech. Dev. 61.199-212(1997).
-!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
EMBL; X99769; CAA68102.1; -.
HSSP; P12643; 3BMP.
                                                                                                                                                                                                                                                                                                                                           412 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZETN; ZBS-GENE-980526-442; gdf6a.
InterPro; IPR002400; GF_cysknot.
InterPro; IPR001839; TGFb.
InterPro; IPR001111; TGFb.N.
Pfam; PF00019; TGF-beta; 1.
Pfam; PF00688; TGFb_propeptide; 1.
PRINTS; PR00438; GFCZKNOT.
PRODO; PR00037; TGFb; 1.
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412 AA; 47072 MW;
                                                                                                                                                                                                                                                                                                                                                                                           Dynamo protein precursor.
                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=7955;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-EMBRYO;
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                                                                                     152 VSMLSDKEELVGAELRLFRQAPSAPWGPPAGPLHVQLFPCLSPLLLDARTLDPQGAPPAG 211
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                                                                                                                                                         284 HSKTRRSRRTALPNRHGKRSKSKCSKKPLHVNFRELGWDDWVIAPLDYEAYHCEGM
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                                                                                                                                                                                                                                                                                           WEVFDVWQGLR----HQPWKQLCLELRAAWGELDAGEAEARARGPQQPPPDLRSLGFGR
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
                                 34;
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 Length 412;
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                                 71; Indels
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5F1B0D7D97E591F6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DB 13;
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44.6%; Score 1091.5; DB 59.1%; Pred. No. 1.6e-79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    413 AA
                                 46; Mismatches
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PROSITE; PS00250; TGF_BETA_1; 1.
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                                 Matches 218; Conservative
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Matches 211; Conservative
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                 Similarity
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Q9BDW8
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                                                                                                           77 AQQPRAQEPPGRGPRVVPHEYMLSIYRTYSIAEKLGINASFFQSSKSANTITSFVDRGLD 136
                                                                                                                                                                    137 DLSHTPLRRQKYLFDVSMLSDKEELVGAELRLFRQAP - - SAPWGPPAGPLHVQLFPC - - 191
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                                                                                                                                                                                                                                                                                             170 WQEPKLIDSRPADLLDTVFSKWEVFNVWKAVGNRRLSGETLCFMLKI-----VSDIKAT 223
                                                                                                                                                                                                                                                                                                                                           307
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                                                                                                                                                                                                                                                                                                                                                                                                                          308 GAEGSWPPPSGAPDARPWLPSPGRRRRRTAFASR--HGKRHGKKSRLRCSKKPLHVNFKE 365
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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                                                                                                                                                                                                                                                                                                                                      249 ARGPQQPPPPDLRSLGFGRRVRPPQERALLVVFTRSQRK-NLFAEMREQLGSAEAAGPGA
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 36.9%; Score 902; DB 13; I
Best Local Similarity 44.2%; Pred. No. 3.2e-64;
Matches 204; Conservative 69; Mismatches 129;
                                       13 LWSAWLWAAAAASGLLSSHRLRLTGGAR-RAIATLHGHPKD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 500 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            interPro; IPR001405; Inhibin_alpha.
InterPro; IPR001819; TGPD.
InterPro; IPR001111; TGPD_N.
Pfam; PP00019; TGF-beta; 1.
Pfam; PF00688; TGF-beta; 1.
Pfam; PF00689; TGF-beta; 1.
ProDom; P0000357; TGFb; 1.
SMART; SM00204; TGFB; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GDF-5 protein.
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                                                            REGQEPQPRPQDEPRAQQPRAQEPPGRGPRVVPHEYMLSIYRTYSIAEKLGINASFFQSS 121
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     61
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DTPRVLLSAVFLISFLWDLPGFQQASISSSCSSAELGSTKGMRSRKEGKMQRAPRDSDAG
                                                                                                                                                                                                                                                 G--PLHVQLFPC----LSPLLLDARTLDPQGAPPAGWEVFDVWQGLRH-QPWKQLCLELR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAWGELDAGEAEARARGPQQPPPPDLRSLGFGRRVRPPQERALLVVFTRSQRKNL-FAEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    354 CSKKPLHVNFKELGWDDWIIAPLEYEAYHCEGVCDFPLRSHLEPTNHAIIQTLMNSMDPG
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Welkaryota; Metacoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Cercopithecus; Cercopithecus; Cercopithecus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | [1] | SEQUENCE FROM N.A. | SEQUENCE FROM N.A. | Matakabe A., Fujita H., Hayashi M., Yamamori T.; | Watakabe A., Fujita H., Hayashi M., Yamamori T.; | Growth/differentiation factor 7 is preferentially exp | Growth/differentiation factor 7 is preferentially exp | Growth/differentiation factor 7 is preferentially exp | Signary motor area of the monkey neocortex."; | J. Neurochem. 76:1455-1464 (2001). | -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY. | REMEL, AF254568; AAK30842.1; | -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY. | REMEL, AF254568; AAK30842.1; | JOINED. | REMEL; PLS043; 38MP. | RICHEPTO: IPRO01311; TGFD. | REMEL TGF-BETA FAMILY. | RICHEPTO: IPRO01311; TGFD. | REMEL TGF-BETA FAMILY. | RICHEPTO: IPRO01311; TGFD. | REMEL TGF-BETA FAMILY. | REMEL TGF
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STPPSCCVPTKLTPISILYIDAGNNVVYKQYEDMVVESCGCR 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     447 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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Pfam; PF00088; TGFb_propeptide;
ProDom; PD000357; TGFb; 1.
SMART; SM00204; TGFB; 1.
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SEQUENCE 4
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                                                                                                                                                                               GSAEAAGPGAGAEGSWPPPSGAPDARPWLPSPGRRRRTAFASRH------GKRHGK 348
                                                                                                                                                                                                                      01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Growth differentiation factor 5 (Fragment).
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                        191
                                                             184
                                                                                   --LSPLLLDARTLDPQGAPPAGWEVFDVWQGLRH-----QPWKQLCLELRAAWGELDAGE 244
                                                                                                                           245 AEARARGPQQPPPPDLRSLGF---GRRVRPPQERALLVVFTRSQRK-NLFAEMREQ---L 297
                                                                                                                                                                                                           349 KSRLRCSKKPLHVNFKELGWDDWIIAPLEYEAYHCEGVCDFPLRSHLEPTNHAIIQTLMN 408
RAQQPRAQEPPG-RGPRVVPHEYMLSIYRTYSIAEKLGINASFFQSSKSANTITSFVDRG 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-LEG BUD;

MEDLINE-99119368; PubMed=9918693;

MEDLINE-99119368; PubMed=9918693;

Merino R., Macias D., Ganan Y., Fornomides A.N., Wang X., Wu Q.,

A stall N., Sampath K.T., Vazona P., Hurle J.M.;

Expression and function of Gdf-5 during digit skeletogenesis in the mbryonic chick leg bud.";

Tembryonic chick leg bud.";

L. Dev. Biol. 206:33-45(199).

C. '- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.

REMBL, AF075441; AAD14568.1; ...

RESP: P12643; 3BMP.

RICEPPO: IPRO01405; Inhibin_alpha.

RICEPPO: IPRO0111; TGFb.

R Pfam; PF00019; TGF-beta; 1.

R Pfam; PF00019; TGF-beta; 1.

R Pfam; PF00069; INHIBINA.

R PROMOSS; TGF).

R PROMOSS; TGF).
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                                         LDDLSHTPLRRQKYLFDVSMLSDKEELVGAELRLFRQAPSAPW-GPPAGPLHVQLFPC--
                                                   51;
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                                                                                                                                                                                                                                                    409 SMDPGSTPPSCCVPTKLTPISILYIDAGNNVVYKQYEDMVVESCGCR 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0B8A7CB111375007 CRC64;
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324 AA; 37206 MW;
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                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00204; TGFB; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9031;
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NON_TER 32
NON_TER 32
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Q9YHW9
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92 VVPHEYMLSIYRTYSIAEKLGINASFFQSSKSANTITSFVDRGLDDLSHTPLRRQKYLFD 151

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     324 PWLPS--PGRRRRTAFASRHGKRHGKKSRLRCSKKPLHVNFKELGWDDWIIAPLEYEAY 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         164 AELRLFRQAPSAPW-GPPAGPLHVQLFPC----LSPLLLDARTLDPQGAPPAGWEVFDVW 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QGLRH-----QPWKQLCLELRAAWGELDAGEAEARARGPQQPPPPDLRSLGF---GRRVR 270
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TISSUB-CEREBARAL CORTEX MOTOR AREA;
MEDILINE-21136583; PubMed=11238730;
Watakabe A., Fujita H., Hayashi M., Yamamori T.;
"Growth/differentiation factor 7 is preferentially expressed in the primary motor area of the monkey neocortex.";
J. Neurochem. 76:1455-1464(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VSMLSDKEELVGAELRLFRQAPSAPWGPPAG--PLHVQLFPC----LSPLLLDARTLDPQ
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last amnotation update)
01-Orth/differentiation factor 7 (Fragment).
Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Macaca sessional Macaca, Chordata, Craniata, Vertebrata, Buteleostoml;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Glycoprotein.

NON_TER 1 1 SEQUENCE 294 AA; 31792 MW; 49B7BCD9F27AF39F CRC64;
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KQYEE
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SEQUENCE FROM N.A. MEDLINE=99148135; PubMed=10022976; MEDLINE=99148135; PubMed=10022976; Davidson A.J., Postlethwait J.H., Yan Y.L., Beier D.R., van Doren C., Foernzler D., Celeste A.J., Crosier K.E., Crosier P.S.; Isolation of zebrafish gdf7 and comparative genetic mapping of genes belonging to the Growth/Differentiation factor 5, 6, 7 subgroup of the
                                                                                                          --LLHSRAAEPLGG--ARWEAFDVTDA 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        242 AGEAEARARGPQQPPPPDLRSLGFGRRVRPPQERALLVVFTRSQRK-NLFAEMREQLGSA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Brachydanio rerio (Zebrafish) (Zebra danio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostoml;
Actinopterygil; Neopterygil; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxID=7955;
                                                   210 VQSHRRWPRASRKFCLVLRA----VTASESS------PLALRRLGFGWPGGGDGGG
                                                                                           270 RPPQERALLVVFTRSQRK-NLFAEMREQLGSAEAAGPGAGAEGSWPPPSGAPDARPWLPS
                                                                                                                                                                     362 NFKELGWDDWIIAPLEYEAYHCEGVCDFPLRSHLEPTNHAIIQTLMNSMDPGSTPPSCCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             194 PLLLDART---LDPQGAPPAGWEVFDVWQGLRHQPWKQ------LCLELRAAWGELD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PLLLSSRTIDLLDLLDTSSATWDVFDVGPIK-TPLKQHRTAEDTRLLCLSISA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Score 698.5; DB 13; Length 261;
; Pred. No. 3e-48;
28; Mismatches 56; Indels 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LR-HQPW----KQLCLELRAAWGELDAGEAEARARGPQQPPPPDLRSLGFG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE 261 AA; 29414 MW; 77346E977036A104 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Growth/differentiation factor 7 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genome Res. 9:121-129(1999).
-!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
EMBL; AF113023; AAD20829.1; -.
                                                                                                                                                                                                                                                                                                                                                                               261 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR002400; GF_Gysknot.
InterPro; IPR002400; GF_Gysknot.
InterPro; IPR001405; Inhibin_alpha.
InterPro; IPR001839; TGFb.
Fram; PR0019; TGF-beta; 1.
PRINTS; PR00438; GFCYSKNOT.
PRINTS; PR00669; INHIBINA.
PRODOM; PD0000357; TGFb; 1.
    162 PDRDSATLLPRLLLSTCPDEAGTAH----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PS00250; TGF_BETA_1; 1.
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ZFIN; ZDB-GENE-990714-1; gdf7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 153; Conservative
                                                                                                                                                    329 -PGRRRRRTAFASRH----
                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                         422 PTKLTPISILYIDA 435
                                                                                                                                                                                                                                                                                          TGF-beta superfamily.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Glycoprotein.
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                                  221
                                                                                                                                                                                                                                           368
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                                                                                                                 271 PPQERALLVVFTRSQRK-NLFAEMREQ---LGSAEAAGPGAGAEGSWPPPSGAPDARPWL 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 GRE-GQEPQPRPQDEPRAQQPRA-QEPPGRGPR---VVPHEYMLSIYRTYSIAEKLGINA 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SFFQSSKSANTITSFVDRGLDDLSHTPLRRQKYLFDVSMLSDKEELVGAELRLFRQAPSA 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P------WGPPAGPLHVQLFPCLSPLLLDARTLDPQGAPPAGWEVFDVWQG 220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Watakabe A., Fujita H., Hayashi M., Yamamori T., "Growth/differentiation factor 7 is preferentially expressed in the
                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                  PSPGRRRRTAFASRH * * * * * - * - * - GKRHGKKSRLRCSKKPLHVNFKELGWDDWIJAPLE
                                                                           1 MDLSAAAALCLWLLSACRPRDGLEAAAVLRAAGAGPAWS--------PGGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MDTPRVLLSAVFLISFLWDLPGFQQASISSSCSSAELGSTKGMRSRKEGKMQRAPRDSDA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45617 MW; 74DA312A853701F0 CRC64;
                                                                                                                                                                                                                                                                                                                             17, Last sequence update)
21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28.8%; Score 705; DB 11; I 38.1%; Pred. No. 1.7e-48; ive 53; Mismatches 141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       primary motor area of the monkey neocortex.";
J. Neurochem. 76:1455-1464(2001).
-!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                            7 (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSSP, P12643; 3BMP.
InterPro; IPR002405; Inhibin_alpha.
InterPro; IPR00189; TGFb.
InterPro; IPR001111; TGFb.
Pfam; PF00619; TGF-beta; 1.
Pfam; PF00688; TGFb_propeptide; 1.
PRINTS; PR00669; INHIBINA.
ProDom; PD000357; TGFB; 1.
                                                                                                                                                                                                                                                                                                            01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=TT2;
MEDLINE=21136583; PubMed=11238730;
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                                                                                                                                                                                                                                                                                                                                                            Growth/differentiation factor
                                                                                                                                                                             NVVYKQYEDMVVESCGCR 455
                                                                                                                                                                                             Best_Local Similarity 38.1%
Matches 188; Conservative
                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                               (TrEMBLrel.
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NON_TER 441
SEQUENCE 441
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-I- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.

EMBL: Y12005; CAA72733.1; ---

HSSP: P12643; 3BMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :: : | | : | : | | 10 KS-----RRFSNPIPEHSIKGHP----RRRRRATALAGRPGVGPITSGGKGGGRRRIR 159
                                                                                                              160 CSRKPLHVNFKELGWDDWIIAPLDYEAYHCEGLCDFPLRSHLEPTNHAIIQTLMNSMDPE 219
                                                                                               CSKKPLHVNFKELGWDDWIIAPLEYEAYHCEGVCDFPLRSHLEPTNHAIIQTLMNSMDPG 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          186 VQLFPCLS----PLLLDARTLDPQGAPPAGWEVFDVW---QGLRHQPWKQLCLELRAAWG 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120 -----GKKPIKNPKQRCNRK 159
58 VSDSNNEAVHPGM-----LGLSREDOOTHERALLVAFSOARRKENLFREIREKIRAM 109
                               301 EAAGPGAGGEGSWPPPSGAPDARPWLPSPGRRRRRTAFASR-----HGKRHGKKSRLR 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        239 ELDAGEAEARARGPQQPPPPDLRSLGFGRRVRPPQERALLVVFTRSQRKNLF-AEMREQL 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        298 GSAEAAGPGAGAEGSWPPPSGAPDARPWLPSPGRRRRRTAFASRHGKRHGKRSRLRCSKK 357
                                                                                                                                                                                                                                                                                                                                                                                  Brachydanio rerio (Zebrafish) (Zebra danio).
Eukaryota: Metazoa: Chordata: Craniata; Vertebrata; Euteleostomi;
Actinopterygil; Neopterygil; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 13; Length 257;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27.2%; Score 664.5; DB 13; Length
51.8%; Pred. No. 1.6e-45;
tive 32; Mismatches 53; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
6D64F0542F948849 CRC64;
                                                                                                                                                                                                                                                                                                       01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                             STPPSCCVPTKLTPISILYIDAGNNVVYKQYEDMVVESCGCR 455
                                                                                                                                                                            220 STPPSCCVPSKLSPISILYIDSGNNVVYKQYEDMVVESCGCR 261
                                                                                                                                                                                                                                                                            257 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZFIN; ZDB-GENE-990415-39; gdf5.
InterPro; IPR002400; GF_cysknot.
InterPro; IPR001839; TGFb.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00250; TGF_BETA_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            257 AA; 29787 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00019; TGF-beta; 1. PRINTS; PR00438; GFCYSKNOT. ProDom; PD000357; TGFb; 1. SMART; SM00204; TGFB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 144; Conservative
                                                                                                                                                                                                                                                                            PRELIMINARY;
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257
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                                                                                                                                                                                                                                                                                                                                                         Contact (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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NON_TER
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042303
                                                                                             354
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Lee K.J., Mendelsohn M., Jessell T.M.; "Neuronal patterning by BMPs: a requirement for GDF7 in the generation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      331 RRRRRTAFASRHGKR-HGKKSRLRCSKKPLHVNFKELGWDDWIIAPLEYEAYHCEGVCDF 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lytechinus variegatus (Sea urchin).
Eukaryota, Metazoa, Echinodermata, Eleutherozoa, Echinozoa,
Echinoidea, Euechinoidea, Echinacea, Temnopleuroida, Toxopneustidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of a discrete class of commissural interneurons in the mouse spinal cord.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25.0%; Score 612.5; DB 13; Length 126; 86.5%; Pred. No. 1e-41;
                                                                                                                                                                                                                                                                01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Putative growth/differentiation factor 6/7 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE 126 AA; 14265 MW; CB824D280F44A394 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
SCCVPTKLTPISILYIDAGNNVVYKQYEDMVVESCGCR 455
                           220 TCCVPTRLSPISILYIDSANNVYKQYEDMVVESCGCR 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genes Dev. 12:3394-3407(1998).
-!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
HSSP; P12643; 3BAP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Pred. No. 1e-41; 10; Mismatches
                                                                                                                                                                                        126 AA
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                                                                                                                                                                                                                                          01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequ
01-JUN-2002 (TrEMBLrel. 21, Last anno
                                                                                                                                                                                     PRT;
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InterPro; IPR002405; Inhibin_alpha.
InterPro; IPR001839; TGFb.
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MEDLINE=99026113; PubMed=9808626;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00250; TGF_BETA_1; 1.
Glycoprotein.
NON_TER 1
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PRINTS; PR00438; GFCYSKNOT.
PRINTS; PR00669; INHIBINA.
ProDom; PD000357; TGFB; 1.
SMART; SM00204; TGFB; 1.
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Matches 109; Conservative
                                                                                                                                                                                        PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                             Gallus gallus (Chicken)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ESCGCR 455
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Q9XYQ7;
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MEDLINE=21850182; PubMed=11862464;
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             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                        132 DRGLDDLSHTPLRRQKYLFDVSMLSDKEELVGAELRLFR------QAPSAPWGPPAG 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                75 PRAQQPRAQEPPGRGPRVVPHEYMLSIYRTYSIAEKLGINASF---FQSSKSANTITSFV 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KRHGKKSRLRCSKKPLHVNFKELGWDDWIIAPLEYEAYHCEGVCDFPLRSHLEPTNHAII 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  306 KRKGKRLKANCRRHPLYVDFSDVHWNDWIVAPAGYQAYYCHGECPFPLAEHLNTTNHAIV 365
                                                                                                                                                                                                                                                                                                                            01-MAR-2002 (TrEWBLrel. 20, Created)
01-MAR-2002 (TrEWBLrel. 20, Last sequence update)
01-JUN-2002 (TrEWBLrel. 21, Last annotation update)
Anti-dorsalizing morphogenetic protein.
Brachydanio rerio (Zebrafish) (Zebra danio).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; NCBI_TAXID-7955;
                                                                                                                                                                                                                                                                                                            21 PGFQQASISSSCSSAELGSTKGMRSRKEGKMQRAPRDSDA-----GREGQEPQPRPQDE 74
                             Angerer L.M., Oleksyn D.W., Logan C.Y., McClay D.R., Dale L., Angerer R.C.; "A BMP pathway regulates cell fate allocation along the sea urchin animal-vegetal embryonic axis.";
                                                                                                                                                                                                                                                                                                                                                                                                                     : | | :|::| : :| | | ||11|||| : : 119 HEDAGQVLPTEHHHTVIFNISTMPAEEVLTMAELRLFRKDLEEHSIAKRHALDDRKSLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PLH----VQLFPCLSPL-----LLDARTLDPQGAPPAGWEVFDV-----WQGLRH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                224 QPWKQLCLELRAAWGELDAGEAEARARGPQQPPPPDLRSLGFGRRVRPPQERALLVVFTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SQRKNLFAEMREQLGSAEAAGPGAGAEGSWPPPSGAPDARPWLPSPGRRRRTAFASRHG
                                                                                                                                                                                                                                                                                        Indels 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QTLMNSMDPGSTPPSCCVPTKLTPISILYIDAGNNVVYKQYEDMVVESCGCR 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 417;
                                                                           Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
EMBL: AAD28038.1; -.
HSSP: P12643; 3BMP.
                                                                                                                                                                                                                                         417 AA; 47727 MW; 5EB93E3022BFC50F CRC64;
                                                                                                                                                                                                                                                               20.7%; Score 507; DB 5; L. 30.1%; Pred. No. 1.2e-32; tive 72; Mismatches 142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        391 AA
                                                                                                                      InterPro; IPR002405; Inhibin_alpha.
InterPro; IPR001839; TGFb.
InterPro; IPR001131; TGFb.N.
Pfam; PF00019; TGF-beta; I.
Pfam; PF000189; TGF_beta; I.
PRINTS; PR00669; INHIBINA.
PRODOM; PD000337; TGFb; I.
PROSITE; PS00250; TGFB; I.
PROSITE; PS00250; TGFB; I.
                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                            Local Similarity
                     SEQUENCE FROM N.A
NCBI_TaxID=7654;
                                                                                                                                                                                                                                                                                      Matches 142;
                                                                                                                                                                                                                                          SEQUENCE
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17;
                                                      "Expression of the anti-dorsalizing morphogenetic protein gene in the zebrafish embryo.";
Dev. Genes Evol. 211:568-572(2001).
EMBL; AR420475, AAL60179.1; -.
InterPro; IPR001839; TGFb.
InterPro; IPR001111; TGFb_N.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         83 QEPPGRGPRVVPHEYMLSIYRTYSIAEKLGINASFFQSSKSANTITSFVDRGLDDLSHTP 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            143 LRRQKYLFDVSMLSDKEELVGAELRLFRQAPSAPWGPPAGPLHVQLFPCLSPL-LLDA-- 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 21, Last annotation update)
Anti-dorsalizing morphogenetic protein annotation oralic (Zebrafish) (Zebra danio).
Brachydanio rerio (Zebrafish) (Zebra danio).
Bukaryota: Metazoa: Chordata; Craniata: Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
NCBI_TAXID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             303 AGPGAGAEGSWPPPSGAPDARPWLPSPGRRRRRTAFASRHGKRHGKKSRLRCSKKPLHVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             244 EAEARARGPQQPPPPDLRSLGFGR-RVRPPQERALLVVFTRSQRKNLFAEMREQLGSAEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     245 ASLEATSKGSDVSPGGSSQPLPSVPASRRSSRSVDYDER----GEK--MACQRQPLYVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              363 FKELGWDDWIIAPLEYEAYHCEGVCDFPLRSHLEPTNHAIIQTLMNS--MDPGSTPPSCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   79;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 391;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65; Mismatches 125; Indels
Dickmeis T., Rastegar S., Aanstad P., Clark M., Fischer Straehle U.;
                                                                                                                                                                                                                            Pfam; PF00019; TGF-beta; 1.
Pfam; PF00688; TGFD_propeptide; 1.
ProDom; PD000357; TGFD; 1.
SMART; SM00249; TGFB; 1.
PROSITE; PS00250; TGF_BETA_1; UNKNOWN_1.
SEQUENCE 391 AA; 43769 MW; F17F83652C34962B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                         18.7%; Score 457.5; DB 1.31.9%; Pred. No. 1.1e-28;
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Glycoprotein
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                                                                                                                                                                                                           143 LRRQKYLFDVSMLSDKEELVGAELRLFRQAPSAPWGPPAGPLHVQLFPCLSPL-LLDA-- 199
                                                                                                                                                                                                                                                                        | :||::| :: |::||| ||: |
104 -ERIEYLFUMSTVAKSEKILTAELHLFKLRPKT----SIVLNRHHFCQVSVYQVLDSSK 157
                                                                                                                                                                                                                                                                                                                                    302
                                                                                                                                                                                                                                                                                                                                                                                                                 244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 245 ASLEATSKGSDVSPGGXSQPLPSVPASRRSSRSVDYDER----GEK--MACQRQPLYVD 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          363 FKELGWDDWIIAPLEYEAYHCEGVCDFPLRSHLEPTNHAIIQTLMNS--MDPGSTPPSCC 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----RTLDPQGAP--PAGWEVFDVWQGLRHQPWKQ-----LCLELRAAWGELDAG
                                                                                                                                                                                                                                                                                                                                                                                244 EAEARARGPQQPPPPDLRSLGFGR-RVRPPQERALLVVFTRSQRKNLFAEMREQLGSAEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. Knoechel W.; Knoechel W.; Rroechel S., Dillinger K., Koester M., Knoechel W.; "Structure and expression of Xenopus tropicalis BMP-2 and BMP-4
                                                                                                                             DB 13; Length 391;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   genes.";
submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
EMBL, AJ315160; CAC44178.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Knochel W.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases
InterPro; IPR001111; TGFb_N.
Pfam; PF00019; TGF-beta; 1.
Pfam; PF00688; TGFb_Propeptide; 1.
Pr000m; PD000237; TGFb; 1.
PROSITE; PS00226; TGFB; 1.
PROSITE; PS00250; TGF_BETA_1; UNKNOWN_1.
SEQUENCE 391 AA; 43792 MW; F89885D22364962B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Bone morphogenetic protein 2.
                                                                                                                           18.7%; Score 456.5; DB 13; ilarity 31.9%; Pred. No. 1.3e-28; Conservative 64; Mismatches 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     421 VPTKLTPISILYIDAGNNVVYKQYEDMVVESCGCR 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       357 VPDKLYSISLLYFDDDENVVLKQYDDMVAGSCGCR 391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam: PF00019; TGF-beta; 1.
Pfam: PF00018; TGF-beta; 1.
Probom: PD000357; TGFb; 1.
PROSITE; PS00250; TGF_BETA_1; UNKNOWN_1.
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InterPro; IPR001111; TGFb_N.
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                                                                                                                                            Best Local Similarity
Matches 126; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                             86 PGRGPRVVPHEYMLSIYRTYS--IAEKLGINASFFQ---SSKSANTITSF-VDRGLDDLS 139
                                                                                                                                                                                                                                          140 HTPLRR-QKYLFDVSMLSDKEELVGAELRLFRQAPSAPWGPPAGPLH-VQLFPCLSPL-- 195
                                                                                                                                                                                                                                                                      243 GEAEARARGPQQPPPDLRSLGFGRRVRP----PQERALLVVFTRSQRKNLFAEMREQL 297
                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     237 -----NDKNVPKKHVR---ISRSLVPDKDSWPRIRPLLVTFSHD------
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                                                                                                                                                                                                                                                                                                                                                                                     185 ASRGPVVRLLDTRLIHHN---ESKWESFDVTPAITRWIAHKQPNHGFVVEVT----HLD-
                                                                                          96;
                                               Length 398;
                                                                                               117; Indels
50AF783E4A529146 CRC64;
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                                             Score 453; DB 13;
Pred. No. 2.5e-28;
                                                                                             68; Mismatches
45437 MW;
                                             18.5%;
29.8%;
                                                                                             Matches 119; Conservative
398 AA;
                                          Query Match
Best Local Similarity
SEQUENCE
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Search completed: November 25, 2002, 02:57:55 Job time : 94 secs

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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
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OM protein - protein search, using sw model

November 25, 2002, 02:33:40; Search time 37 Seconds (without alignments) 510.047 Million cell updates/sec Run on:

US-09-825-751A-20 2447 1 MDFPRVLLSAVFLISFLWDL.......GNNVVYKQYEDMVVESCGCR 455 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

112892 seqs, 41476328 residues Searched:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	P55106 bos taurus	homo	P43027 mus musculu	P43028 mus musculu	P43029 mus musculu	P25703 xenopus lae	34 xenopus	52	oryctol	P12644 homo sapien		P49001 rattus norv	Q06826 rattus norv					P21274 mus musculu	Q29607 dama dama (mus m	095393 homo sapien	gallu		homo	xenop	P34821 mus musculu	P30886 xenopus lae	_	P91699 drosophila	P18075 homo sapien	Snm 6	954	P07713 drosophila
SUMMARIES	TD	GDF6_BOVIN	GDF5_HUMAN	GDF5_MOUSE	GDF6_MOUSE	GDF7_MOUSE	BMPA_XENLA	BMPB_XENLA	BMP4_CHICK	BMP2_RABIT	BMP4_HUMAN	BMP4_MOUSE	BMP2_RAT	BMP4_RAT	BMP2_HUMAN	BMP4_RABIT	DVR1_STRPU	BMP2_DAMDA	BMP2_MOUSE	BMP4_DAMDA	BMP5_MOUSE	BM10_HUMAN	BMP2_CHICK	BMP8_HUMAN	BMP5_HUMAN	BMP4_XENLA	BM8A_MOUSE	BMP7_XENLA	BM10_MOUSE	DECA_DROPS	BMP7_HUMAN	BMP7_MOUSE		DECA_DROME
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DECA_DROSI BMF6_MOUSE BMF6_HUMAN UTV_STRPU GDF2_HUMAN DECA_TRICA DSL1_CHICK BMBB_MOUSE BM3B_RAT	BM3B_HUMAN DVR1_BRARE
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ALIGNMENTS

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                                             Gaps
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                                                                                              TISSUE-Articular cartilage;
MEDIINE=95050604; PubMed=7961761;
Chang S., Hoang B., Thomas J.T., Vukicevic S., Luyten F.P.,
Ryba N.J.P., Kozak C.A., Reddi A.H., Moos M.;
"Cartilage-derived morphogenetic proteins. New members of the transforming growth factor-beta superfamily predominantly expressed in long bones during human embryonic development.";
J. Biol. Chem. 269:28227-28234(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hoetten G., Neidhardt H., Jacobowsky B., Pohl J.;
Kloning and expression of recombinant human growth/differentiation
factor 5.";
                                                                            SSAELGSTKGMRSRKEGKMQRAPRDSDAGRE---GQEPQPRPQDEPR---AQQPRAQEPP
                                                                                                                                                                                                                                                                                                   GRRVRPPQERALLVVFTRSQRKNLFAEMREQLGSA-EAAGPGAGAEGSW------PPPPS
                                                                                                                                                                                                                                                                                                                                                                    GAPDARPWLPSPGRRRRTAFASRHGKRHGKKSRLRCSKKPLHVNFKELGWDDWIIAPLE
                                                                                                                                                                                                                                                                                                                                                                                                                                   147 KYLFDVSMLSDKEELVGAELRLFRQAPSAPWGPPAGPLHVQLFPCLSPLLLDARTLDPQG
                                                                                                                                                                                                                                                                                  APPAGWEVFDVWQGLRHQPWKQLCLELRAAW-GELDAGEAEARARGPQQPPPPDLRSLGF
                                             18;
             Length 436;
                                             Indels
                                           48;
        73.5%; Score 1798; DB 1;
80.8%; Pred. No. 4.2e-113;
tive 18; Mismatches 48;
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MEDLINE~21638749; PubMed=11780052;
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MEDLINE-95071375; PubMed-7980526;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 354; Conservative
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                          Similarity
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            Query Match
Best Local S
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A Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Buck D., Burill W.D., Butler A.P., Carder C., Carter N.P.,
Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Coulson A., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M.,
Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Howden P.J.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA W.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
Lehvaslaiho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
Marsh V.L., Martin S.L., McConnachie L.J., McLay K., McMurray A.A.,
Allilimore B.J.C.T., Prathallingam S.R., Plumb R.W., Ramsay H.,
RA Phillimore B.J.C.T., Prathallingam S.R., Plumb R.W., Ramsay H.,
RA Swunc C.D., Smith M.L., Scott C.E., Sehra H.K., Shownkeen R., Sims S.,
Race C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims S.,
Race C.M., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
RA Wilming L., Wray P.W., Hubbard T., Williams L., Williams S.A.,
RA Milming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Rogers J..,
RA Rogers J.,
RA Rogers R.,
RA Rogers J.,
RA Rogers J.,
RA Roger
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T -> S (IN REF. 2).
APGGG -> VPRSR (IN REF. 2).
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PROSITE; PS00250; TGF_BETA_1; 1.
Signal; Growth factor; Cytokine; Glycoprotein.
SIGNAL
Deloukas P., Matthews L.H., Ashurst J.,
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ProDom; PD000357; TGFb; 1.
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InterPro; IPR001111; TGFb_N.
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Pfam; PF00688; TGFb_prope
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Genew; HGNC:4220; (
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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Nature 368:639-643(1994).
-! FUNCTION: COULD BE INVOLVED IN BONE FORMATION.
-! SUBUNIT: HOWODIMER; DISULFIDE-LINKED (BY SIMILARITY).
-! SUBUNIT: HOWODIMER; DISULFIDE-LINKED (BY SIMILARITY).
-! DISEASE: DEFECTS IN GDF5 ARE THE CAUSE OF BRACHYPODISM WHICH ALERS THE LENGTH AND NUMBERS OF BONES IN THE LIMBS BUT SPARES THE
                                                                                                                                    -----PRAQEPPGRGPRVVPHEYMLSIYRTYSIAEKLGINASFFQ 119
                                                                                                                                                                                           174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       407
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                                                                                               Gaps
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MEDILNE-94195427; PubMed-8145850;
Storm E.E., Huynh T.V., Copeland N.G., Jenkins N.A., Kingsley D.M.,
Lee S.-J.;
                                                                                                                                                                                                                                              -APWGPPAGPLHVQLFPCLS----PLLLDARTLDPQGAPPAGWEVFDVWQGLRH-QPWKQ
                                                                                                                                                                                                                                                                                                                AAPGGGRAAQL - - KLSSCPSGRQPASLLDVRSV - - PGLDGSGWEVFDIWKLFRNFKNSAQ
                                                                                                                                                                                                                                                                                                                                           LCLELRAAWGELDAGEAEARARGPQQPPPPDLRSLGFGRRVRPPQERALLVVFTRSQRKN
                                                                                                                                                                                                                                                                                                                                                             KKSRLRCSKKPLHVNFKELGWDDWIIAPLEYEAYHCEGVCDFPLRSHLEPTNHAIIQTLM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus.
                                                                                             97;
                                                                    501;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NSMDPGSTPPSCCVPTKLTPISILYIDAGNNVVYKQYEDMVVESCGCR 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
                                                                                             Indels
S -> A (IN REF. 2).
A -> T (IN REF. 2).
L -> S (IN REF. 2).
; 37985F2D15C4F5EF CRC64;
                                                                  , DB 1;
.4e-55;
les 98;
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01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Growth/differentiation factor 5 precursor (GDF-5)
GDF5 OR BDF.
Mus musculus (Mouse)
                                                                                                                      GSTKGMRSRKEGKMQRAPRDSDAGREGQEPQPRPQDEPRAQQ --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AXIAL SKELETON.
-!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A
                                                                                            64; Mismatches
                                                                  37.9%; Score 927.5; 44.7%; Pred. No. 5.4
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                                       55410 MW;
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Mammalia; Eutheria; Rodentia;
                                                                 Query Match 37.9
Best Local Similarity 44.7
Matches 209; Conservative
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276
321
384
                                       501 AA;
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SEQUENCE FROM N.A.
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            CONFLICT
CONFLICT
SEQUENCE
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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S -> P.
CDOD5DE48185D2E3 CRC64;
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GROWTH/DIFFERENTIATION FACTOR 5
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
                                                                                                                                                                                                           Cytokine; Glycoprotein; Polymorphism.
                                                                                                                                                                                                                                                                                                                                                 37.6%; Score 919.5; DB 1; Length 43.5%; Pred. No. 1.8e-54; ive 74; Mismatches 107; Indels
European Bioinformatics Institute. The by non-profit institutions as long
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                                                                                       MGD, MGI.95688, Gdf5.
InterPro; IPR001400; GF_cysknot.
InterPro; IPR001400; GF_cysknot.
InterPro; IPR001111; TGFb.
InterPro; IPR001111; TGFb.
Pfam; PF00019; TGFb_beta; I.
Pfam; PF00688; TGFb_propeptide; I.
Probom; PD000387; TGFb_ropeptide; I.
SMART; SM00249; TGFB; I.
SMART; SM00240; TGFB; I.
SHOSITE; PS00250; TGFB:I.
SHOSITE; PS00250; TGF_BETA_1; I.
SHOMAL; Growth factor.
SIGNAL
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495
495
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54885 MW;
                                                                   EMBL; U08337; AAA18778.1;
HSSP; P12643; 3BMP.
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GDF6_MOUSE

RESULT 4

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Growth/differentiation factor 7 precursor (GDF-7) (Fragment)
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BMPA_XENLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        331 RRRRRTAFASRHGKRHGKKSRLRCSKKPLHVNFKELGWDDWIIAPLEYEAYHCEGVCDFP 390
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STRAIN-BALB/c; TISSUE-Liver;
MEDLINE-94195427; Pubmed-8145850;
Storm E.E., Huynh T.V., Copeland N.G., Jenkins N.A., Kingsley D.M.,
                                                                                                                                                 Eukaryota; Metaria; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBL_raxID=10090;
                                                                                                                                                                                                                                                                                                                                        "Limb alterations in brachypodism mice due to mutations in a new
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BY SIMILARITY.
BY SIMILARITY.
SIMILARITY.
INTERCHAIN (BY SIMILARITY).
10FA2A5B7748DA32 CRC64;
                                       01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Growth/differentiation factor 6 precursor (GDF-6) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28.2%; Score 691; DB 1; Length 12 99.2%; Pred. No. 7.7e-40; ive 1; Mismatches 0; Indels
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(Rel. 32, Last sequence update)
(Rel. 40, Last annotation update)
  125 AA
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PROSITE; PS00250; TGF_BETA_1; 1.
Growth factor; Cytokine; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL
                                                                                                                                                                                                                                                                                                                                                           member of the TGF beta-superfamily.";
Nature 368:639-643(1994).
PRT;
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14373 MW;
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MGD; MGI:95689; Gdf6.
InterPro; IPR001839; TGFb.
Probom; PD00019; TGF beta; 1.
Probom; PD000357; TGFb; 1.
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125 AA;
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                                                                                                                       GDF6 OR GDF-6
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01-NOV-1995 (
16-OCT-2001 (
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hes 124;
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P43029;
  GDF6_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 343 GKRHGKKSRLRCSKKPLHVNFKELGWDDWIIAPLEYEAYHCEGVCDFPLRSHLEPTNHAI 402
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MEDLINE-94195427; PubMed-8145850;
Storm E.E., Huynh T.V., Copeland N.G., Jenkins N.A., Kingsley D.M.,
Lee S.-J.;
                           Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
16-COT-2001 (Rel. 40, Last annotation update)
Bone morphogenetic protain 2-I precursor (BMP-2-I).
Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                        "Limb alterations in brachypodism mice due to mutations in a new member of the TGF beta superfamily."; Nature 368:639-643(1994).
-- SUBGNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
-- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
GROWTH/OFFERENTIATION FACTOR 7.
GROWTH/OFFERENTIATION
BY SIMILARITY.
BY SIMILARITY.
INTERCRAIN (BY SIMILARITY).
POLY-ARG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22.4%; Score 549; DB 1; Length 151; 59.5%; Pred. No. 2.8e-30; ive 13; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0E496AACB5827759 CRC64;
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Growth factor; Cytokine; Glycoprotein.
NON_TER : 1 PROPEP < 5
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Mus musculus (Mouse).
Bukaryota, Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10090;
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MGD; MGI:95690; Gdf7.
InterPro; IPR01839; TGFb.
Pfam; PF00019; TGF* beta; 1.
Probom; P0000357; TGFb: 1.
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116
1148
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115
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Matches 103;
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P25703:
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SEQUENCE
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                                                                                                                               SEQUENCE FROM N.A.

MEDLINE-92378616; PubMed=1510675;

Nishimatsu S., Suzuki A., Shoda A., Murakami K., Ueno N.;

Nishimatsu S., Suzuki A., Shoda A., Murakami K., Ueno N.;

"Genes for bone morphogenetic proteins are differentially transcribed in early amphibian embryos.";

Biochem. Biophys. Res. Commun. 186:1487-1495(1992).

-! FUNCTION: INDUCES CARTILAGE AND BONE FORMATION.

-! SUBUNIT: HOMODIMER; DISULFIDE-LINKED.

-! SUBUNIT: BELONGS TO THE TGF-BETA FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PTPGKNVVIPPYMLDLYHLHLAQLAADEGTSAMDFQMERAASRANTVRSFHHE--ESMEE 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              141 TPLRR----QKYLFDVSMLSDKEELVGAELRLFRQAPSAPWGPPAGPLH-VQLFPCLSPL 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ------LLDARTLDPQGAPPAGWEVFDVWQGL-----RHQPWKQLCLELRAAWGEL 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              183 AAASRGPVVRLLDTRLVHHN---ESKWESFDVTPAIARWIAHKQPNHGFVVEV---NHL 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.

POTENTIAL.

POTENTIAL.

BONE MORPHOGENETIC PROTEIN 2-I.

BY SIMILARITY.

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BY SIMILARITY.

BY SIMILARITY.

INTERCHAIN (BY SIMILARITY).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-Y (IN REF. 2).

N-Y (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SWART; SM00204; TGFB; 1.
PROSITE; PS00250; TGF_BETA_1; 1.
Signal; Growth factor; Cytokine; Bone; Cartilage; Glycoprotein.
                                                                      Plessow S., Koester M., Knoechel W.; "CDNA sequence of Xenopus laevis bone morphogenetic protein 2 \,
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19.2%; Score 471; DB 1; Length 39f
31.1%; Pred. No. 1.2e-24;
tive 60; Mismatches 117; Indels
                                                                                                          Biochim. Biophys. Acta 1089:280-282(1991).
                                                                                                                                                                                                                                                                                                                                                                          PIR; S16244; S16244.
PIR; JH0687, JH0687.
HSSP; P12643; JBMP.
InterPro; IPR001839; TGFb.
InterPro; IPR01111; TGFb.N.
Pfam; PF00019; TGF-Deta; I.
ProDom; PP00088; TGFb_Propeptide; I.
                                                            MEDLINE=91274367; PubMed=2054389;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         45575 MW;
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Conservative (
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3398
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               Kenopodinae; Xenopus
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398 AA;
                                               SEQUENCE FROM N.A.
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Matches 125;
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INTERCHAIN (BY SIMILARITY).

N-LINKED (GLCNAC...) (POTEWIAL).

N-LINKED (GLCNAC...) (POTEWIAL).

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N-LINKED (GLCNAC...) (POTEWIAL).
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                                                                                                                                                                                    296 QLGSAEAAGPGAGAEGSWPPPSGAPDARPWLPSPGRRRRRTAFASRHGKRHGKKSRLR--
                                                                                                                                                                                                                                                                                                                                                                              CSKKPLHVNFKELGWDDWIIAPLEYEAYHCEGVCDFPLRSHLEPTNHAIIQTLMNSMDPG
                                                                                        D------NDKNVPKKHVR---ISRSLTPDKDNWPQIRPLLVTFSHD------
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Xenopus laevis (African clawed frog).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    398 AA.
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InterPro; IPR001839; TGFb.
InterPro; IPR001111; TGFb_N.
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NCBI_TaxID=8355;
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398 AA;
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15-JUL-1999 (
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BMP2_RABIT
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                                                                                                                                                                                                                                                                                       416
                                                                                                                                             242
                                                                                                                                                                                            298
                                                                                                                                                                                                                                         356
                                                                                                                                                                                                                                                       PGRGPRVVPHEYMLSIYRTYS--IAEKLG---INASFFQSSKSANTITSF-VDRGLDDLS 139
                                                                                              HTPLRR-QKYLFDVSMLSDKEELVGAELRLFRQAPSAPWGPPAGPLH-VQLFPCLSPL-- 195
                                                                                                                                                                    241
                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=White leginorn;
STRAIN=White leginorn;
MEDIJINE—94163974; Pubbed=8119128;
Francis P.H., Richardson M.K., Brickell P.M., Tickle C.;
"Bonne morphogenetic proteins and a signalling pathway that controls patterning in the developing chick limb.";
pevelopment 120:209-218(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-99128179; PubMed-9927590; Jazette S., Niswander L.; "BMPs negatively regulate structure and function of the limb apical ectodermal ridge.";
                                                                                                           185 ASRGPVVRLLDTRLIHHN---ESKWESFDVTPAITRWIAHKQPNHGFVVEVTHLDNDTNV
                                                                                                                                                                                         243 GEAEARARGPQOPPPDLRSL----GFGRRVRPPQERALLVVFTRSQRKNLFAEMREQLG
                                                                                                                                           -----LLDARTLDPQGAPPAGWEVFDVWQGL-----RHQPWKQLCLELRAAWGELDA
                                                                                                                                                                                                                                        SAEAAGPGAGAEGSWPPPSGAPDARPWLPSPGRRRRRTAFASRHGKRHGKKSRLR--CSK
                                                                                                                                                                                                         PKRHVRIS------RSLTLDKGHWPRIRP-----LLVTFSHD-------
                                                                                                                                                                                                                                                                                      KPLHVNFKELGWDDWIIAPLEYEAYHCEGVCDFPLRSHLEPTNHAIIQTLMNSMDPGSTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Development 126:883-894(1999).
-!- FUNCTION: NEGATIVELY REGULATES THE STRUCTURE AND FUNCTION OF .
LIMB APICAL ECTODERMAL RIDGE.
-!- SUBUNT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                         94;
 Length 398;
19.0%; Score 464; DB 1; Length 39 30.1%; Pred. No. 3.5e-24; ive 68; Mismatches 117; Indels
                                                                                                                                                                                                                                                                                                                                    PSCCVPTKLTPISILYIDAGNNVVYKQYEDMVVESCGCR 455
                                                                                                                                                                                                                                                                                                                                                360 KACCVPTELSAISMLYLDENEKVVLKNYQDMVVEGCGCR 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bone morphogenetic protein 4 precursor (BMP-4)
                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                       405
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                                                                                                                                                                                                                                                                -----GKGHALH-----
 Query Match 19.0
Best Local Similarity 30.1
Matches 120; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gallus gallus (Chicken)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                    CHICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION
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Q90752;
                                               98
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118 FQSSKS-ANTITSF-VDRGLDDL---SHTPLRRQKYLFDVSMLSDKEELVGAELRLFR-- 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 REGQEPQPRPQDEPRAQQPRAQEPPGRGPRVVPHEYMLSIYRTYSIAEK----LGINASF 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MFGLRRRPQPSKS------AVIP-SYMLDLYRLQSGEEEERSLQEISLQY 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -QAPSAPWGPPAGPLHVQLFPCLSPL-----LLDARTLDPQGAPPAGWEVFDVWQG 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              221 LRHQPWKQLCLELRAAWGELDAGEAEARARGPQQPPPPDLRSLGFGRRVRPPQERALLVV 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---NHGLVIE 237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FASRHGKRHG-KKSRLRCSKKPLHVNFKELGWDDWIIAPLEYEAYHCEGVCDFPLRSHLE 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               238 VTHLHQAQTHQGKHVRISRSLPQGHG----GDW-----AQLRPLLVTFGHDGRGHALTR 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 LLSAVFLISFLWDLPGFQQASISSSCSSAELGSTKGM----RSRKEGKMQRAPRDSDAG 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 MLMVILLCQVL--LGGTNHASLIPETGRKKVAELQGQAGSGRRSAQSHELLRGFETTLLQ 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  397 PINHAIIQTLMNSMDPGSTPPSCCVPTKLTPISILYIDAGNNVVYKQYEDMVVESCGCR 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BY SIMILARITY.

BONE MORPHOGENETIC PROTEIN 4.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

INTERCHAIN (BY SIMILARITY).

N-LINKED (GLCNAC...) (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 453; DB 1; Length 405;
Pred. No. 1.9e-23;
9; Mismatches 162; Indels 110;
                                                                                                                                                                                                                                                             Cartilage; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----SPAVIRWTKDKQP------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 544302DBA0A40F81 CRC64;
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UL-1999 (Rel. 38, Last sequence update)
CT-2001 (Rel. 40, Last annotation update)
Morphogenetic protein 2 precursor (BMP-2)
OR BMP-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      395 AA
email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                      POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                HSSP; P12643; 3BMP.
InterPro; IPR0011839; TGFb.
InterPro; IPR001111; TGFb_N.
Pfam; PF00019; TGF-beta; I.
Pfam; PF00688; TGFb_propeptide; I.
ProDom; PD000357; TGFb; I.
                                                                                                                                                                                                         SMART; SM00204; TGFB; 1.
PROSITE; PS00250; TGF_BETA_1; 1.
Signal; Growth factor; Cytokine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46057 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18.5%;
28.8%;
                                          EMBL; X75915; CAA53514.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                405
370
402
404
369
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                292
3305
3334
344
208
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20;

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REPAIR.
                                                                                                                                                                                     BMP4_HUMAN
   387
                                                                    447
                                                                                                                                                                                                                                                                                                            Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --RREKRQA------KHKQRKRLKSSCKRHPLYVDFSDVGWNDWIVAPPGYHAFYCHGE 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     87
                                                                                                                             Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION (BY SIMILARITY).
-!- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.

BY SIMILARITY.

BONE MORPHOGENETIC PROTEIN 2.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

INTERCHAIN (BY SIMILARITY).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ASSGR----PSPQPSDDILSEFELRLLSMFGLKQRPTPSRDAVVP-PYMLDLYRRHS--G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ELQVFREQMQEALGDDSGFHHRINIYEIIKPATANSKFPATRLLDTRLVNQN---TSRWE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SFDVTPAVMR--W-----TAQGHANHGFV-VEVTHLEEKQGVSKRHVRISRSLHPDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PGRRRRRTAFASRHGKRHGKKSRLR--CSKKPLHVNFKELGWDDWIIAPLEYEAYHCEGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  214 VFDVWQGLRHQPWKQLCLELRAAWGELDAGEAEARARGPQQPPPPDLRSLGFGRRVRP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---PQERALLVVFTRSQRKNLFAEMREQLGSAEAAGPGAGAEGSWPPPSGAPDARPWLPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSWSQIRPLLVTF---------GHDGKGHPLH------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bone; Cartilage; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (POTENTIAL)
                                               SEQUENCE FROM N.A. STRAIN-New Zealand white; TISSUE-Ocular ciliary epithelium; Wan X.L., Sears J., Chen S., Sears M.; "Cloning and expression of BMP-2/-4 from rabbit ocular ciliary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 395;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
Eutheria; Lagomorpha; Leporidae; Oryctolagus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8D1DDCFBAC582496 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68; Mismatches 135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18.4%; Score 449.5; DB 1
29.6%; Pred. No. 3.2e-23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                               | Pfan; Pf0019; TGF-beta; 1. |
| Pfan; Pf0068; TGF-beta; 1. |
| Pfan; Pf0068; TGF-beta; 1. |
| PR1078; PR00669; TGFB; 1. |
| Pr0D0m; PD000379; TGFB; 1. |
| SMART; SM00204; TGFB; 1. |
| SMART; SM00204; TGFB; 1. |
| Signal; Growth factor; Cytokine; Bone SIGNAL |
| Signal; Growth factor; Cytokine; Bone SIGNAL |
| Signal; Growth factor; Cytokine; Bone Disulrid |
| Disulrid | 295 360 BY SIMII DISULFID |
| DISULFID | 328 394 BY SIMII DISULFID |
| DISULFID | 359 359 INTERCHE CARBOHYD |
| CARBOHYD | 337 337 N-LINKEL CARBOHYD |
| SIMII DISULEND |
| CARBOHYD | 337 337 N-LINKEL
                                                                                                                                                                                                                                                                                                                                                                  HSSF, P12643; 3BMP.
InterPro; IPR002405; Inhibin_alpha.
InterPro; IPR001839; TGFb.
InterPro; IPR001111; TGFb_N.
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Matches 127; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           295
324
328
359
134
199
337
395 AA;
                   NCBI_TaxID=9986
                                                                                                                   epithelium.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA Seq. 5:273-275(1995).
-!- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION. ALSO ACT IN
MESODERM INDUCTION, TOOTH DEVELOPMENT, LIMB FORMATION AND FRACTURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SUBGENTY: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: SECRETED INTO THE EXTRACELLULAR MATRIX.
-!- TISSUE SPECIFICITY: EXPRESSED IN THE LUNGS AND LOWER LEVELS SEEN IN THE KIDNEY. PRESENT ALSO IN NORMAL AND NEOPLASTIC PROSTATE TISSUES, AND PROSTATE CANCER CELL LINES.
-!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oida S., Iimura T., Maruoka Y., Takeda K., Sasaki S.; "Cloning and sequence of bone morphogenetic protein 4 (BMP-4) from a human placental cDNA library.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shore E.M., Xu M., Shah P.B., Janoff H.B., Hahn G.V., Deardorff M.A. Sovinsky L., Spinner N.B., Zasloff M.A., Wozney J.M., Kaplan F.S.; The human bone morphogenetic protectin 4 (BMP-4) gene: molecular structure and transcriptional regulation."; Calcif. Tissue Int. 63:221-229(1998).
                    CDFPLRSHLEPTNHAIIQTLMNSMDPGSTPPSCCVPTKLTPISILYIDAGNNVVYKQYED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wozney J.M., Rosen V., Celeste A.J., Mitsock L.M., Whitters M.J., Kriz R.W., Hewick R.M., Wang E.A.; "Novel regulators of bone formation: molecular clones and activities."
                                                                                                                                                                                                                                                                                                                                                                        Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Butelo
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                            P12644; Q9UM80;
01-OCT-1989 (Rel. 12, Created)
01-OCT-1989 (Rel. 12, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Bone morphogenetic protein 4 precursor (BMP-4) (BMP-2B).
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Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                              408 AA.
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EMBL; U43842; AAC72278.1; -.
EMBL; BC020546; AAH20546.1; -.
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                                                                                                                                                                                                              STANDARD;
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                                                                        MVVESCGCR 455
                                                                                                             387 MVVEGCGCR 395
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INTERCHAIN (BY SIMILARITY).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).
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                                                           Mans, 114202,
InterPro; IRR001839; TGFb.
InterPro; IRR001111; TGFb_N.
Fam; PF00019; TGF-beta; 1.
Pfam; PF00688; TGFb_propeptide; 1.
Prom; PF0004; TGFB; 1.
SWART; SW00204; TGFB; 1.
PROSITE; PS00250; TGF_BETA_1; 1.
SHART; Growth factor; Cytokine; Bone; Cartilage; Glycoprotein.
SIGNAL.
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Matches 135; Conservative
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                HSSP; P12643; 3BMP.
Genew; HGNC:1071; BMP4.
MIM; 112262; -.
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408 AA;
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P21275;
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MEDLINE-90228966; PubMed-1970330;
Dickinson M.E., Kobrin M.S., Silan C.M., Kingsley D.M., Justice M.J.,
Miller D.A., Ceci J.D., Lock L.F., Lee A., Buchberg A.M.,
Siracusa L.D., Lyons K.M., Derynck R., Hogan B.L.M., Copeland N.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=93365172; PubMed-8358941;
Takaoka K., Yoshikawa H., Hasimoto J., Masuhara K., Miyamoto S.,
Suzuki S., Ono K., Matsui M., Oikawa S., Tsuruoka N.;
Gene cloning and expression of a bone morphogenetic protein derived
from a murine osteosarcoma.";
Clin. Orthop. Relat. Res. 294:344-352(1993).
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                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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--- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION.
--- SUBUNIT: HOWODIMER; DISULFIDE-LINKED (BY SIMILARITY).
--- SUBCELLULAR LOCATION: SECRETED INTO THE EXTRACELLULAR MATRIX.
--- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                           Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                          Dickinson M.E., van der Meer-De Jong R., Hogan B.L.M.;
Submitted (XXX-1992) to the EMBL/GenBank/DDBJ databases
16-OCT-2001 (Rel. 40, Last annotation update)
Bone morphogenetic protein 4 precursor (BMP-4) (BMP-2B)
BMP4 OR BMP-4 OR DVR-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-93282803; PubMed-8507180;
Kurihara T., Kitamura K., Takaoka K., Nakazato H.;
Kurihar Done morphogenetic protein-4 gene: existence o
promoters and exons for the 5'-untranslated region.";
Biochem. Biophys. Res. Commun. 192:1049-1056(1993).
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J. Biol. Chem. 270:28364-28373(1995).
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L47480; AAC37698.1; ALT_INIT.
D14814; BAA03555.1; -.
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Pfam; PF00019; TGF-beta; 1.
Pfam; PF00688; TGFb_propeptide; 1.
ProDom; PD000357; TGFb; 1.
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MEDLINE=96081880; PubMed=7499338;
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InterPro; IPR001839; TGFb.
InterPro; IPR001111; TGFb_N.
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                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                63 EGQEPQPRPQDEPRAQQPRAQEPPGRGPRVVPHEYMLSIYRTYSIAEK-----LGINASF 117
                                                                                                                                                                                                                                                                     107
                                                                                                                                                                                                                                                                                       118 FQSSKS-ANTITSFVDRGLDDLSHTPLRRQ----KYLFDVSMLSDKEELVGAELRLFR-- 170
                                                                                                                                                                                                                                                                                                                              --QAPSAPWG------PPAG--PLHVQLFPCLSPLLLDARTLDPQGAPPAGWEVF 215
                                                                                                                                                                                                                                                                                                                                                                                                           331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     389 FPLRSHLEPTNHAIIQTLMNSMDPGSTPPSCCVPTKLTPISILYIDAGNNVVYKQYEDMV 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                          7 LLSAVFLISFLWDLPGFQQASISSSCSSAELGSTKG-MRSRKEGKMQRAPRDSDA---GR 62
                                                                                                                                                                                                                              64
                                                                                                                                                                                                                                                                                                    DV-----SPAVLR---WTREKOPNYGL
                                                                                                                                                                                                                                                                                                                                                                    DVWQGLRHQPWKQLCLELRAAWGELDAGEAEARARGPQQPPPPDLRSLGFGRRVRPPQER
                                                                                                                                                                                                                                                                                                                                                                                                                             236 AIEVTHLHQTRTHQGQHVRISRSLPQGSGDWA------QLRPLLVTFGHDGRG
                                                                                                                                                                                                                            7 MLMVVLLCQVL--LGGASHASLIPETGKKKVAEIQGHAGGRRSGQSHELLRDFEATLLQM
                                                BONE MORPHOGENETIC PROTEIN 4.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
N-LINKED (GLCNAC...) (POTENTIAL).
C-> S (IN REF. 2).
                                                                                                                                                                                                                                                            166 VDQGPDWEQGFHRINIYEVMKPPAEMVPGH-----LITRLLDTRLVHHN---VTRWETF
                                                                                                                                                                                                                                                                                                                                                                                                         276 ALLVVFTRSQRKNLFAEMREQLGSAEAAGPGAGAEGSWPPPSGAPDARPWLPSPGR----
                                                                                                                                                                                                                                                                                                                                                                                                                                               ---RRRRTAFASRHGKRHGKKSRLRCSKKPLHVNFKELGWDDWIIAPLEYEAYHCEGVCD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                123;
                      Bone; Cartilage; Glycoprotein
                                                                                                                                                                     DB 1; Length 408;
                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (BMP-2A)
                                                                                                                                        -> S (IN REF. 2).
35053D844624EF9D CRC64;
                                                                                                                                                                   17.8%; Score 436.5; DB 1; 28.5%; Pred. No. 2.5e-22; ive 62; Mismatches 163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 precursor (BMP-2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-FEB-1996 (Rel. 33, Last sequence update)
16-007-2001 (Rel. 40, Last annotation update)
BMP2 OR BMP-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                393 AA
                              POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
SMART; SM00204; TGFB; 1.
PROSITE; PS00250; TGF_BETA_1; 1.
Signal; Growth factor; Cytokine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-1996 (Rel. 33, Created)
                                                                                                                                                  Σ.
                                                                                                                                                  46496
                                                                                                                                                                                       Conservative
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                                                                                                                                                 408 AA;
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tes 139; Conserv
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SEQUENCE FROM N.A.
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                                                                   DISULFID
DISULFID
DISULFID
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P49001;
                                                           DISULFID
                                                                                                  CARBOHYD
                                                                                                            CARBOHYD
                                                                                                                     CARBOHYD
                                                                                                                               CARBOHYD
                                                                                                                                                 SEQUENCE
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                                                                                                                                         CONFLICT
                              SIGNAL
                                                                                                                                                                             Best Loca
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          83 QEPPGRGPRVVPHEYMLSIYRTYS-IAEKLGINASFFQSSKSANTITSF-VDRGLDDLSH 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  141 -TPLRRQKYLFDVSMLSDKEELVGAELRLFRQAPSAPWGPPAGPLHVQLFPCLSPL---- 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          418
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   250 RGPQQPPPPDLRSLGFGRRVRPPQERALLVVFTRSQRKNLFAEMREQLGSAEAAGPGAGA 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

INTERCHAIN (BY SIMILARITY).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).
        S.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    251 EHSW-----SQVRPLLVTFGHDGKGHPLHKREKRQA-----KHKQRKRLKSSCKRHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----LLDARTLDPQGAPPAGWEVFDVWQGLRHQPWKQLCLELRAAWGELDAGEAEARA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           182 KFPVTRLLDTRLVTQN---TSQWESFDVTPAVMR--W-----TAQGHTNHGFVVEVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     229 HLEEKP-------GVSKR-------HVRISRSLHOD------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            310 EGSWPPPSGAPDARPWLPSPG-----RRRRRTAFFASRHGKRHGKKSRLR--CSKKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LHVNFKELGWDDWIIAPLEYEAYHCEGVCDFPLRSHLEPTNHAIIQTLMNSMDPGSTPPS
SMART; SM00204; TGFB; 1.
PROSITE; PS00250; TGF_BETA_1; 1.
Signal; Growth factor; Cytokine; Bone; Cartilage; Glycoprotein.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 393;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 434; DB 1; Length 395; Pred. No. 3.5e-22; 62; Mismatches 125; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-LINKED (GLCNAC. . .) (P. 7D20865852E0F213 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BONE MORPHOGENETIC
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Pfam; PF00019; TGF-beta; 1.
Pfam; PF00088; TGFb_propeptide;
Probom; PD000357; TGFb; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44383 MW;
                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; Z25868; CAA81088.1; -.
HSSP; P12643; 3BMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001839; TGFb.
InterPro; IPR001111; TGFb_N.
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              activities
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19;
                                                                                                                                                                      MEDINE-93385188; PubMed-8373807;
Chen D., Feng J.Q., Feng M., Harris M.A., Mundy G.R., Harris S.E.;
"Cloning and sequence of bone morphogenetic protein 4 cDNA from fetal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QQP---RAQEPPGRGPRVVPHEYMLSIYRTYSIAEK----LGINASFFQSSKS-ANTIT 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SFVDRGLDDLSHTPLRRQ----KYLFDVSMLSDKEELVGAELRLFR----QAPSAPWG-- 178
                                                                                                      Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20 LPGFQQASISSSCSSAELGSTKGMRSRKEGKMQRAPRDSDAG--REGGEPQPRPQDEPRA 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bone; Cartilage; Glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 408;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BONE MORPHOGENETIC PROTEIN 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62; Mismatches 168; Indels
                         01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
116-OCT-2001 (Rel. 40, Last annotation update)
Bone morphogenetic protein 4 precursor (BMP-4) (BMP-2B).
BMP4 OR BMP-4 OR DVR-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 4.5e-22;
 A
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 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ProDom; Purvection (1988) 1.
SMART; SM0020; TGFB; 1.
PROSITE; PS00250; TGF_BETA_1; 1.
Signal; Growth factor; Cytokine; Bone;
                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; S33173; S33173.
PIR; S3843; S3843.
RSP; PIS 43843.
InterPro; IPR001839; TGFb.
InterPro; IPR001111; TGFb.
Pfam; PF00019; TGF-beta; I.
Pfam; PF00688; TGFb_propertide; I.
ProDom; PD000357; TGFb; I.
 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46540 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; 222607; CAA80329.1; -.
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Matches 138; Conservative
 STANDARD;
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408
405
407
372
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350
                                                                                          Rattus norvegicus (Rat
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350
365
408 AA;
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DISULFID
DISULFID
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SEQUENCE
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ANDELLINE-21638749; PubMed=11780052;

RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,

RA Jones M., Stavides G., Almeida J.P., Babbage A.K., Bagguley C.L.,

RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,

Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,

RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,

RA Chapman J.C., Clamp M., Clark G., Clark E.Y., Clee C.M.,

RA Chapman J.C., Deddeman R.E., Connor R.E., Corby N.R.,

RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,

RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,

RA Ellington A.G., Frankland J.A., Houte S.E., Jekosch K., Johnson C.M., Johnson D.W.,

RA M.P., Kimberley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,

RA MATSH V.L., Martin S.L., McConnachie L.J., Johnson C.M., Johnson D.M., Leversha M.A., King A., Knights A., Laird G.K., Lawlor S.,

RA Marsh V.L., Martin S.L., McConnachie L.J., McLay K., McMurray A.A.,

Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,

RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,

RA Skuce C.D., Smith M.L., Socht C.E., Sehra H.K., Shownkeen R., Sims S.,

RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,

RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,

RA Tromans A.C. Tromans A.C., Tuddin M., Wall M., Wall H., Hormas D.W., Thorpe A.,

Racey A., Tromans A.C., Tuddin M., Wall M., Wall H., Horley B., Hor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
-----PPAG--PLHVQLFPCLSPLLLDARTLDPQGAPPAGWEVFDVWQGLRHQPWK 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shore E.M., Xu M.-Q., Calvert G., Moriatis J., Kaplan F.S.; "Human bone morphogenetic protein 2 (BMP-2) genomic DNA sequence."; Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              178 RINIYEVMKPPAEMVPGH-----LITRLLDTRLVRHN---VTRWETFDV-----
                                                                                                                                                                                                                                                                                   ----SPAVLR---WTREKOPNYGLAIEVTHLHQTRT
                                                                                                                                                                                                                                                                                                                                                                                   NLFAEMREQLGSAEAAGPGAGAEGSWPPPSGAPDARPWLPSPGR-----RRRRTAFAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        248 HOGOHVRISRSLPOGS-----GNW-----AOLRPLLVTFGHDGRGHTLTRRRAKRSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RHGKRHGKKSRLRCSKKPLHVNFKELGWDDWIIAPLEYEAYHCEGVCDFPLRSHLEPTNH
                                                                                                                                                                                         228 QLCLELRAAWGELDAGEAEARARGPQQPPPPDLRSLGFGRRVRPPQERALLVVFTRSQRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             401 AIIQTLMNSMDPGSTPPSCCVPTKLTPISILYIDAGNNVVYKQYEDMVVESCGCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ol-OCT-1989 (Rel. 12, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Bone morphogenetic protein 2 precursor (BMP-2) (BMP-2A). BMP2 OR BMP2A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 396 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Rel. 12, Created)
(Rel. 12, Last seq
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BMP2_HUMAN
BMP2_HUMAN
DT 01-0CT-
DT 01-0CT-
DT 15-JUN-
DT 15-JUN-
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Pfam; PF00688; TGFD-propeptide; 1.
Prodom; PD000357; TGFD; 1.
SMART; SM0204; TGFB; 1.
PROSITE; PS00250; TGF_BETA_1; 1.
PROSITE; PS00250; TGF_BETA_1; 1.
SIGNAL: 1 1 19
                                                                                                                                                                                                                                                                                                       372 LYLDENEKVVLKNYQDMVVEGCGCR 396
                                                                                             --GVSKR------HVRISRSLHQD
                                                                                                                                                                                                                                                                                    LYIDAGNNVVYKQYEDMVVESCGCR
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InterPro; IPR001111; TGFb.N.
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309
338
342
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351
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046576;
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CHAIN
DISULFID
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20;
                                                                                                                                                                           J. MOL. Biol. 287:103-115(1999).
-!- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION.
-!- SUBUNIT: HOMODIMER; DISULFIDE-LINKED.
-!- TISSUE SPECIFICITY: PARTICULARLY ABUNDANT IN LUNG, SPLEEN AND COLON AND IN LOW BUT SIGNIFICANT LEVELS IN HEART, BRAIN, PLACENTA, LIVER, SKELETAL MUSCLE, KIDNEY, PANCREAS, PROSTATE, OVARY AND SMALL INTESTINE.
P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49 GKMQRAPRDSDAGREGQEPQPRPQDEPRAQQP-----RAQEPPGRGPRVVPHEYMLS 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IYRTYSIAEKLGINAS-----FFQSSKSANTITSF-VDRGLDDLSHTPLR-RQKYLFDV 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             202 LDPQGAPPAGWEVFDVWQGLRHQPWKQLCLELRAAWGELDAGEAEARARGPQQPPPPDLR 261
                                      20.";
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                                                                                                                                                 2.7 A
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N-LINKED (GLCNAC. . .) (POTENTIAL).

20653A3987B25E60 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001111; TGFb_N.
Pfam; PF00019; TGF-beta; 1.
Pfam; PF00089; TGF-beta; 1.
ProDom; PD000357; TGFb; 1.
SMART; SM00204; TGFB; 1.
PROSITE; PS00250; TGF_BETA_1; 1.
Signal; Growth factor; Cytokine; Bone; Cartilage; Glycoprotein;
                                    comparative analysis of human chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 396;
                                                                                                         MEDLINE-99175323; PubMd-10074410;
Scheufler C., Sebald W., Huelsmeyer M.;
"Crystal structure of human bone morphogenetic protein-2 at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BONE MORPHOGENETIC PROTEIN 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17.6%; Score 431.5; DB 1; 29.2%; Pred. No. 5.1e-22; ive 67; Mismatches 139;
                                                                                           X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 292-396
                                                                                                                                                                                                                                                                                                                   SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF040249; AAF21646.1; --
EMBL; AL035668; CAB82007.1; --
PIR; B37278; B37278.
PDB; 3BMP; 12-MAR-00.
Genew; HGNC.1069; BMP2.
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                                                      Nature 414:865-871(2001).
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361
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163
164
                                      sequence and
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200
396 AA;
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Best Local Similarity
Wilming L., Wray
Roqers J.;
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329
360
135
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SIGNAL
                                                                                                                                                                     resolution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            130;
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DISULFID
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321
                                                                                                                                                                                                                                                                                                                              SIMILARITY).
                                                                                                                                                                                       SLGFGRRVRPPQERALLVVFTRSQRKNLFAEMREQLGSAEAAGPGAGAEGSWPPPSGAPD
                                                                                                                                          322 ARPWLPSPG-----RRRRTAFASRHGKRHGKKSRLR--CSKKPLHVNFKELGWDD
                                                                                                                                                                                                                                                                                     WIIAPLEYEAYHCEGVCDFPLRSHLEPTNHAIIQTLMNSMDPGSTPPSCCVPTKLTPISI
                                                                       -----SQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -i- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION (BY SIMILARITY E SUBMIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
-i- SUBCELLULAR LOCATION: SECRETED INTO THE EXTRACELLULAR MATRIX.
-i- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
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N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. STRAIN-New Zealand white; TISSUE-Ocular ciliary epithelium; Wan X.L., Sears J., Chen S., Sears M.; "Cloning and expression of BMP-2/-4 from rabbit ocular ciliary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
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BONE MORPHOGENETIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Bone morphogenetic protein 4 precursor (BMP-4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                   63 EGQEPQPRPQDEPRAQQPRAQEPPGRGPRVVPHEYMLSIYRTYSIAEKL-----GINA 115
                                                                                                                                                                                                            116 SFFQSSKSANTITSF-VDRGLDDLSHTPLRRQ-KYLFDVSMLSDKEELVGAELRLFRQAP 173
                                                                                                                                                                                                                                                                             108 PERPASR-ANTVRSFHHEEHLENIPGTSENSAFRFLFNLSSIPENEAISSAELRLFRE-- 164
                                                                                                                                                                                                                                                                                                                            174 SAPWGP--PAGPLHVQLFPCLSP------LLLDARTLDPQGAPPAGWEVFDVWQG 220
                                                                                                                                                                                                                                                                                                                                                                                            221 LRHQPWKQLCLELRAAWGELDAGEAEARARGPQQPPPPDLRSLGFGRRVRPPQERALLVV 280
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                                             Ouery Match 17.6%; Score 430; DB 1; Length 409; Best Local Similarity 27.7%; Pred. No. 6.7e-22; Matches 134; Conservative 68; Mismatches 167; Indels 114; Gaps
                                                                                                                     7 LLSAVFLISFLWDLPGFQQASISSSCSSAELGSTKG-MRSRKEGKMQRAPRDSDA---GR 62
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November 25, 2002, 00:20:15 : Search time 3689 Seconds (without alignments) 11241.935 Million cell updates/sec
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Maximum Match 1008
Listing first 45 summaries
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1 Vernet,C.A., Burgess,C.E., Fernandes,E., Taupier,R.J., Quinn,K.E., Spytek,K.A., Rastelli,L. and Herrmann,J.L. Novel proteins and nucleic acids encoding same

Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

PAT 29-OCT-2001

linear

DNA

AX277361 1425 bp Sequence 19 from Patent W00174897. AX277361 4X277361.1 GI:16548926

RESULT 1
AX277361
LOCUS
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human.

REFERENCE . AUTHORS

TITLE

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Zerhusen, B.D., Padigaru, M., Spytek, K.A., Spaderna, S.K., Gangolii, E.A., Rastelli, L., Burgess, C.E., Majumder, K., Shimkets, R., Mishra, V., Vernet, C.A., Szekeres, E.S., Grosse, W.M., Alsobrook, J.P., Liu, X., Gerlach, V.L., Ellerman, K., Smithson, G., Peyman, J., Stone, D. Proteins and nucleic acids encoding the same
Patent: WO 0214368-A 19 21-FEB-2002;
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Patent: WO 0194587-A 15 13-DEC-2001;
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Pred. No. 3.9e-215;
0; Mismatches 0;
                                   /note="unnamed protein product"
/organism="Homo sapiens"
/db_xref="taxon:9606"
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Duery Match 99.8%; Score 1421.8; DB 6; Length 2791; Matches 1423; Conservative 0; Mismatches 2; Indels 0; Gaps 1 CTCTGGGGAGACGCAGTTGCCCGCATGGATACTCCCAGGTCCTCTCGCC 60	DESCRIPTION OF THE PROPERTY	361 CTGGGCATCAATGCCAGCTTTTTCCAGTCGTCAAGTCGGCTAATACGATCACCAGCTTT 420	1539 CAGGGGCCCTCAGGGGGCCACCAGCGGGCCGCTCCAGGGGGGCCGCCCTCTGTTTTTTTT	1779 GACCCCAGCACCCCCGGACCTCGGACCTCGCCCGACCTCGCCCGCGAGGGTGCGGGTTTTCGCCCCGCGAGGGTGCGGGTTTCGCCCCGCGAGGGTGCGGGTTTCGCCCCGGAGGGTGCGGGTTTTCGCCCCGGAGGGTGCGGGTTTCGCCCCGGAGGGTGCGGGGGGGG

kerly, R. Boguslavkiy, L., Boukhgalter, B., ngelo, M., Collins, S., Collymore, A., Collymore, A., Collymore, R., Collins, S., Collymore, R., Collins, C., Collins, R., Collins, R., Collins, R., Collins, R., Collins, R., Collins, R., Kerstas, A., Klein, J., Ke, K., Macdonald, P., Marquis, N., Macdonald, P., Marquis, N., Macdonald, P., Connor, T., O'Donnell, P., Riley, R., Suy, A., Santos, R., Severy, P., Collins, R., Suy, A., Santos, R., Severy, P., Collins, R., Wheeler, J., Wu, X., A. and Zody, M. baum,C., Lander,E., Allen,N., Anderson,S., uslavkiy,L., Boukhgalter,B., Brown,A., Cooke,P., Choepel,Y., Colangelo,M., Gooke,P., DeArellano,K., Dewar,K., S., Ferreira,P., FitzHugh,W., Gage,D., inde,S., Goyette,M., Graham,L., Heaford,A., Horton,L., Hulme,W., es,C., Karatas,A., LarRocque,K., Lehoczky,J., Levine,R., Liu,G., Marquis,N., Matthews,C., McCarthy,M., cpheeters,R., Meldrim,J., Meneus,L., PRI 01-MAY-2001 a; Craniata; Vertebrata; Euteleostomi; s; Catarrhini; Hominidae; Homo. cehead Institute/MIT Center for Genome
c. Cambridge, MA 02141, USA CGCCATCATCCAGACGCTCATGAACTCCATG 1260 GIGCCCACCAAATIGACTCCCATCAGCATT 1320 CTACAAGCAGTACGAGGACATGGTGGTGGAG 1380 CTACAAGCAGTACGAGGACATGGTGGTGGAG 2378 3 bp DNA linear J14, complete sequence. CGCCGCCTTGGCCCG 1425 CGCCGCCTTGGCCCG 2423 um, C. and Lander, E. J14

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                                                                                                                                                                                                                                                                                                   rpt_family="L1MA4A"
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2329. .12362
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850
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complement(8208.
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21514. .22019
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Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Nell,D., Oliver,J., Peterson,K., Phukkhang,P., Pierre,N., Pollara,V., Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R., Seaman,S., Severy,P., Sougneaz,C., Spencer,B., Stange-Thomann,N., Stojanovic,M., Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Travers,M., Travis,N., Trigilio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

Li Submitted (Q1-MAY-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA on Mar 21, 2001 this sequence version replaced gi:11560231.
                                                                                                                                                                                                                                                                                                                                                                 Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
Center project name: L3477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Web site: http://www-seq.wi.mit.edu
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1. 156873
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7699. .7917

/rpt_family="LIMB3"

complement(7920. .8214)
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3807. .3911
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6492. .6595
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599. .1763
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complement(2665. ..
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Direct Submission
Submitted (03-APR-2001) Nobuyoshi Shimizu, Keio University, School
of Medicine, Molecular Biology; 35 Shinanomachi, Shinjuku-ku, Tokyo
160-8882, Japan (E-mall:Inshimizudemb.med.keto.ac.jp,
Tel:81-3-3351-2370, Fax:81-3-3351-2370)
on May 28, 2001 this sequence version replaced gi:13646601.
Location/Qualifiers
1. 230879
/Organism="Homo sapiens"
/db_xref="Hoxon:9606"
/chromosome="8"
                                                                                                                                                                                                                                                                 nrvvJ+vJ
HOMO sapiens genomic DNA, chromosome 8q23, clone:KB1043D8.
AP003465
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104633 CCGCCCAGCTGCTGCCTGCCACCACCAATGACTCCCATCAGCATTCTATACATCGACGC 104574
                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                Db 104573 GGGCAATAATGTGGTCTACAAGCAGTACGAGGACATGGTGGTGGAGTCGTGCGGCTGCAG 104514
                                                         1335 GGGCAATAATGTGGTCTACAAGCAGTACGAGGACATGGTGGTGGAGTCGTGCGGCTGCAG
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Shimizu, N. and Asakawa, S.
Homo sapiens DNA chromosome 8 SEQUENCE
Published Only in Database (2001)
2 (bases 1 to 230879)
Shimizu, N. and Asakawa, S.
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/clone_lib="Keio BAC library"
335. .404
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/evidence=not_experimental
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/rpt_family="MIR"
485. .1418
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/rpt_family="L2"
complement(1500. .1704)
                                                                                                                                                           Db 104513 GTAGCGGTGCCTTTCCCGCCGCCCTTGGCCCG 104483
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complement(7991. .8748)
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                                                                                                                                                                                                                                                                                                                                                                                                clone:KB1043D8.
Homo sapiens
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     104693 GGAGCCCACCAACAACCACCCATCATCCAGACGCTGATGAACTCCATGGACCCCGGCTCCAC
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                                                                                                                                                                                                                                       DB 9;
                                                                                                                                                                                                                                                                         0; Mismatches
  .23045)
                                                                                                                                                                                                                                       Score 991;
Pred. No. 4
                                                 /rpt_family="L2"
23166. 23357
/rpt_family="MLTIJ2"
23404. 23532
/rpt_family="MLTIJ2"
23544. 23749
/rpt_family="L2"
23785. 24246
                  /rpt_family="MLT1A1"
23046. .23137
complement (22990.
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Matches 991; Conservative (
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repeat_region	family="MER20" 10869
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repeat_region	521 Idence
repeat_region	<pre>/rpt_family="(TGAA)n" complement(1474215115)</pre>
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repeat_region	59561
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repeat_region	1717917309
	/evidence=not_experimental /rpt_familv="MER94"
repeat_region	1848318503
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repeat_region	39692
	/evidence=not_experimental /rpt_family="MIR"
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/rpt_family="MIR" 29490. 29536 /evidence=not experimental	/rpt_family="(GA)n" 30171. 30193 /evidence=not_experimental	/rpt_ramily="Gt_rich" 3021530269 /evidence=not_experimental /rpt_family="GC_rich"	3110131412 /evidence=not_experimental /rpt_family="L2"	3192731953 /evidence=not_experimental /rot_family="(CA)n"	31953. 31979 /evidence=not_experimental	/rpt_ramily="(GA)n" complement(3280232978) contence=not_experimental	<pre>/ipt_lamily= mix complement(3370233866) /evidence=not_experimental</pre>	/rpt_family="MER5A" 3483934884	/rpt_family="L1MA8" 34890, .34916	/evidence=not_experimental /rpt_family="AT_rich"	<pre>complement(3495435023) /evidence=not_experimental ////////////////////////////////////</pre>	<pre>/rpt_ramily*"Mik" complement(3570535923) /evidence=not experimental</pre>	/rpt_family="MIR" complement(3653136718)	/evidence=not_experimental /rpt_family="MIR"	<pre>3/0083/226 /evidence=not_experimental /rot_familv="MIR"</pre>	3954839568 /evidence=not_experimental	/rpt_family="GC_rich" 4160041706	<pre>/evidence=not_experimental /rpt_family="(TC)n" 4216842400</pre>	<pre>/evidence=not_experimental /rpt_family="MIR" 4444044511</pre>	/evidence=not_experimental /rpt_family="CT-rich" 4528445340	/evidence=not_experimental /rpt_family="GA-rich" 4611346158	/evidence=not_experimental /rpt_family="G-rich" 4623746291	/evidence=not_experimental /rpt_family="GC_rich" 4691847077	/evidence=not_experimental /rpt_family="CT-rich" complement(4734347520)	ch 69.5%; Score 991; DB 1 Similarity 100.0%; Pred. No. 4e- 991; Conservative 0; Mismatches
repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat region	, . ı	repeat_region	repeat_region	repeat_region		repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	Query Match Best Local Similar Matches 991; Cor

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07-OCT-1997

PAT

DNA

1171 bp 162379 1171 bp Sequence 25 from patent US 5658882.

162379

LOCUS

RESULT 6 I62379

Rosen, V.A., Wolfman, N.M., Thomsen, G.H. 1038 1218 487 787 367 427 Gaps 67 439 GATCTCGCACACTCCTCCGGAGACAGAAGTATTTGTTTGATGTGTCCATGCTCTCA GACAAAGAAGAGCTGGTGGGCGCGGAGCTGCGGCTCTTTCGCCAGGCGCCCTCAGCGCCCC CTGCTGGTGGTATTCACCAGATCCCAGCGCAAGAACCTGTTCGCAGAGATGCGCGAGCAG GAGTACGAGGCCTATCACTGCGAGGGTGTATGCGACTTCCCGCTGCGCTCGCACCTGGAG TGGGGGCCACCAGCGGGCCGCTCCACGTGCAGCTCTTCCCTTGCCTTTCGCCCCTACTG GTGTGGCAGGCCCTGCGCCCACCAGCCTGGAAGCAGCTGTGCTTGGAGCTGCGGGCCGCA CCCCCGGACCTGCGGAGTCTGGGCTTCGGCCGGAGGGTGCGGCCTCCCCAGGAGCGGGCC CTGGGCTCGGCCGAGGCTGCGGGCCCGGGCGCGGGCGCCGAGGGGTCGTGGCCGCCGCCG AAGCCCCTGCACGTGAACTTCAAGGAGCTGGGCTGGGACGACTGGATTATCGCGCCCCTG AAGCCCCTGCACGTGAACTTCAAGGAGCTGGGCTGGGACGACTGGATTATCGCGCCCCTG 1 (bases 1 to 1171)
Celeste, A.J., Wozney, J.M., Rosen, V.A., Wolfman, N.M., Thom and Melton, D.A.
Methods of inducting formation of tendon and/or ligament comprising administering BMP-12, BMP-13, and/or MP-52
Patent: US 5658882-A 25 19-AUG-1997; .; 0 Length 1171; Score 987; DB 6; Le Pred. No. 4.1e-146; ö Mismatches Location/Qualifiers /organism="unknown" 384 c 413 g 69.3%; Scc. 100.0%; Pre 0; GI:2480327 Conservative Unclassified Similarity ď 899 728 g g

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Matches 956; Conservative
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                                                                                                                                                                                                                                                                                                                                                                          AC126226 184987 bp DNA linear HTG 04-JUL-2002 Papio cynocephalus anubis clone RP41-394G6, WORKING DRAFT SEQUENCE, 3 unordered pieces.
    1278
                                                                1338
                                                                                                                           1339 AATAATGTGGTCTACAAGCAGTACGAGGACATGGTGGTGGAGTCGTGCGGCTGCAGGTAG 1398
                                                                                             907
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Center project Information

Center clone name: 94c6

Center clone name: 94c6

Sequencing vector: plasmid: n/a; 100% of reads
Sequencing vector: plasmid: n/a; 100% of reads
Chemistry: De-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990319

Consensus quality: 183965 bases at least Q40

Consensus quality: 183965 bases at least Q30

Consensus quality: 183965 bases at least Q30

Insert size: 177000; agarose-fp

Insert size: 177000; agarose-fp

Insert size: 184787; sum-of-contigs

Quality coverage: 9.00x in Q20 bases; sum-of-contigs
788 CCCACCAACCACGCCATCATCCAGACGCTGATGAACTCCATGGACCCCGGCTCCACCCC
                                                              CCCAGCTGCTGCGCCCCACCAAATTGACTCCCATCAGCATTCTATACATCGACGCGGGC
                                                                               Direct Submission
Submitted (04-JUL-2002) NIH Intramural Sequencing Center,
Grovemont Circle, Gaithersburg, MD 20877, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      * NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        arbitrary. Gaps between the contigs are represented as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center: NIH Intramural Sequencing Center
Center code: NISC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Web site: http://www.nisc.nih.gov
                                                                                                                                                                                        1399 CGGTGCCTTTCCCGCCGCCTTGGCCCG 1425
                                                                                                                                                                                                         968 CGGTGCCTTTCCCGCCCTTGGCCCG 994
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                                                                                                                                                                                                                                                                                                                  DEFINITION
 1219
                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE
JOURNAL
REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE
JOURNAL
                                                            1279
                                                                                                                                                                                                                                                                                                                                                   ACCESSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUTHORS
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                                                                                                                                                                                                                                                                    RESULT 7
AC126226
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KEYWORDS
SOURCE
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Db 178750 CGACGTGTGGCAGGGGCTGCCCACCAGCCCTGGAAGCAGCTGTGCTTGGAGCTGCGGGGC 178809
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Db 178870 GCGCCCCCGGACCTGCGGAGTCTGGGCTTCGGCCGGAGGGTGCGGCCCCCTCAGGAGC 178929
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runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Db 178630 GCCTTGGGGGCCACTAGCCGGGCCGCTCCACGTGCACTTTCCGTGCCTTTCGCCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGCCCTGCTGGTGTATTCACCAGATCCCAGCGCAAGAACCTGTTCGCAGAGATGCGCGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            555 GCCCTGGGGGCCACCAGCCGGGCCGCTCCACGTGCAGCTCTTCCCTTGCCTTTCGCCCT
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                                                                                                    40078: contig of 40078 bp in length
40178: gap of unknown length
111588: contig of 71410 bp in length
111688: gap of unknown length
184987: contig of 73299 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                201 others
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    .184987
    /organism="Papio cynocephalus anubis"
/db_xref="taxon:9555"
    /clone="RP41-39466"

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96.5%; Pred. No. 2.8e-138;
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40179. .111588
//note="assembly_fragment"
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/note="assembly_fragment
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1 (bases 1 to 1308)
Chang, S.C., Hoang, B., Thomas, J.T., Vukicevic, S., Luyten, F.P., Ryba, N.J., Rozak (C.A., Reddl, A.H. and Moss, M. Jr.

Ryba, N.J., Rozak (C.A., Reddl, A.H. and Moss, M. Jr.

Cartilage-derived morphogenetic proteins. New members of the transforming growth factor-beta superfamily predominantly expressed in long bones during human embryonic development

J. Biol. Chem. 269 (45), 28227-28234 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (16-AUG-1994) Malcolm Moos, FDA/CBER, 1401 Rockville Pike (HFM-527), Rockville, MD 20852-1448, USA
On Jan 24, 1995 this sequence version replaced gi:600733.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fprotein_id="AaA61416.1"
| Dis.xref="G1:632490"
| Aranslation="RASAELGSAKGNRTRKEGRMPRAPRENATAREPLDRGEPPRPQ
| EEPQRRPPQQPEAREPPGRGPRLVPHEYMLSIYRTYSIAEKLGINASFFQSSKSANTI
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                                                           179170 CAAGAAGCCCTTGCACGTGAACTTCAAAGAGCTGGGCTGGGACGACTGGATTATGCGCC 179229
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                                                                                                       CCTGGAGTACGAGGCCTATCACTGCGAGGGTGTATGCGACTTCCCGCTGCGCTCGCACT
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                                             CAAGAAGCCCCTGCACGTGAACTTCAAGGAGCTGGGCTGGGACGACTGGATTATCGCGCC
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/tissue_type="articular cartilage"
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2 (bases 1 to 1308)
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ALRLPVAPAAGSAEFGPAGAPRGWEVFDVWRGLRPQPWKQLCLELRAAWGGEPGAAE
BEARTPGPOPPDLRSLGFGRRVPRPQERALLVVFSRSQRKTLFARMREQLGSATE
VUGAGGGAEGGSPPPPPPPPPGBRALLVVFSRSQRKTLFARMREQLGSATE
CSKKPLHVNFKELGWDWIIAPLEYEAYHCEGVCDFPLRSHLEPTNNAIIQTLMNSWD
PGSTPPSCCYPTKLTPISILYIDAGNNVYNEYEEMVVESCGCR"
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/gene="CDMP-2"
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Pred. No. 7.3e-137;
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/gene="CDMP-2"
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Spytek, K.A., Rastelli, L. and Herrmann, J.L.
Novel proteins and nucleic acids encoding s
Patent: WO 0174897-A 84 11-OCT-2001;
Curagen Corporation (US)
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/db_xref="taxon:9913"
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                                          GGGCGCCGAGAGAATGCCACGGCCCGGGAGCCCCTGGATCGCCAGGAGCCCCCGCCGA
                      GGCCTCAGGACGACCC--;-----CGGGCTCAGCAGCCCCGGGCGCAGGAGCCGCCAG
                                                                                                                                AGTATITGITTGATGTGTCCATGCTCTCAGACAAGAAGAGGCTGGTGGGCGCGCGGAGCTGC
                                                                                                                                         AGCTCTTCCCTTGCCTTTCGCCCCTACTGCTGGACGCGCGGGACCCTGGACCCGCAGGGGG
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                                                                                                                                                                                                                                                                    143312 bp DNA linear HTG 04-JUL-2002 -410H13, WORKING DRAFT SEQUENCE, 7 unordered
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
1 (bases 1 to 143312)
1283 GCTGCTGCGGTGCCCACCAAATTGACTCCCATCAGCATTCTATACATCGACGCGGGCAATA 1342
                                             1196 GCTGCTGCGTGCCCACCAAATTGACTCCCATCAGCATCTTGTACATCGACGCGGGCAATA 1255
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Sequencing vector: plasmid: n/a: 100% of reads
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 140814 bases at least Q40
Consensus quality: 141226 bases at least Q30
Consensus quality: 14128 bases at least Q20
Insert size: 142000; agarose-fp
Insert size: 14210; sun-of-contigs
Quality coverage: 9.96x in Q20 bases; sum-of-contigs
Quality coverage: 9.91x in Q20 bases; sum-of-contigs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (04-JUL-2002) NIH Intramural Sequencing Center,
Grovemont Circle, Galthersburg, MD 20877, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NOTE: This is a 'working draft' sequence. It currently consists of 7 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                         1256 ATGTGGTCTACAACGAGTACGAGGAGATGGTGGAGGTGGAGTCGTGCGGCTGCAGC 1308
                                                                                             1343 AFGTGGTCTACAAGCAGTACGAGGACATGGTGGTGGAGTCGTGCGGCTGCAGG 1395
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2917: gap of unknown length
17821: contig of 14904 bp in length
17921: gap of unknown length
37586: contig of 19665 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center code: NISC
Web site: http://www.nisc.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: nisc_zoo@nhgri.nih.gov ------ Project Information
                                                                                                                                                                                                                                                                                           Felis catus clone RP86-410H13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center clone name: 410H13
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AC126238.1 GI:21693902
HTG; HTGS_PHASE1; HTGS_DRAFT.
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2 (bases 1 to 143312)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3;
587 37686: gap of unknown length (687 55500: contig of 18814 bp in length (501 56600: gap of unknown length (7514: contig of 19114 bp in length (715 75814: gap of unknown length (815 10953: gap of unknown length (19454 143312: contig of 33859 bp in length (100453: gap of unknown length (1946) (1941312: contig of 33859 bp in length)
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Pred. No. 1.6e-130;
0; Mismatches 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="assembly_fragment"
31312 c 30631 g 40835 t
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1. .2817
/note="assembly_fragment"
2918. .17821
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17922. .37586
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109454. .143312
                                                                                                                                                             /organism="Felis catus"
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                                                                                                                                                                                                                                                                                                                                                                        vector_side:right"
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94.0%;
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Matches 933; Conservative
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arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
Sequencing vector: plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990319 consensus quality: 213653 bases at least Q40 Consensus quality: 215481 bases at least Q30 Consensus quality: 215481 bases at least Q20 Insert size: 209000; agarose-fp sum-of-contigs Quality coverage: 7.79x in Q20 bases; agarose-fp Quality coverage: 7.79x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                     NOTE: This is a 'working draft' sequence. It currently consists of 12 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                           3801: contig of 3801 bp in length 3901: gap of unknown length 6418: contig of 2517 bp in length 6518: gap of unknown length 12134: contig of 5616 bp in length 12234: gap of unknown length 8170: contig of 5836 bp in length 8170: contig of 19584 bp in length 754: contig of 19584 bp in length 754: gap of unknown length 754: gap of unknown length 04: contig of 19880 bp in 4; contig of 19880 bp in 7: contig of unknown length 7: contig
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="assembly_fragment" 37855. 57704
/note="assembly_fragment
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155373. .183289
/note="assembly_fragment"
183390. .219978
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/db_xref="taxon:9913"
/clone="RP42-416E22"
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gap of
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1. .3801
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155272:
155372:
183289:
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1 (Dases 1 to 219978)

2 Akhter, N., Antonellis, A., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Boutfard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Idol, J.R., Karlins, E., Laric, P., Heghighi, P., Hansen, N., Ho, S.-L., Idol, J.R., Karlins, E., Laric, P., Margulies, E.H., Masiello, C., Maduro, V.B., Matrian, S.D., McCloskey, J.C., McDowell, J., Paguirigan, C., Pearson, R., Portnoy, M.E., Prasad, A., Schueler, M.G., Stantripop, S., Thomas, J.W., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D. In Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HTG 04-JUL-2002
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Bos taurus clone RP42-416E22, WORKING DRAFT SEQUENCE, 12 unordered
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                                                                                        1032 GCGCACGCCTTCGCCAGTCGCCATGGCAAGCGGCACGCCAAGAAGTCCAGGCTACGCTG 1091
                                                                                                                                                                             1092 CAGCAAGAAGCCCCTGCACGTCAAGGAGCTGGGCTGGGACGACTGGATTATCGC 1151
                                                                                                                                                                                                                                                                                                                                                                1212 CCTGGAGCCCACCAACCACGCCATCATCCAGACGCTGATGAACTCCATGGACCCCGGCTC 1271
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972 GCCGCCGTCGGGCCCCCGGATGCCAGGCCTTGGCTGCCCTCGCCCGGCCGCCGGCGGCG 1031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (04-JUL-2002) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gaithersburg, MD 20877, USA
                          51045 CAGCAAGAAGCCCCTGCACGTGAACTTCAAGGAGCTGGGCTGGGACGACTGGATTATCGC
                                                                                                                                                                                                                                                                        GCCCCTGGAGTACGAGGCCTATCACTGCGAGGTGTATGCGACTTCCCGCTGCGCTCGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                        1272 CACCCCCCCAGCTGCTGCGTGCCCACCAAATTGACTCCCCATCAGCATTCTATACATCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center: NIH Intramural Sequencing Center
Center code: NISC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Web site: http://www.nisc.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51345 CAGGTAGCGGCCCTTCCTGCTGCCTTGGCCC 51377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1392 CAGGTAGCGGTGCCTTTCCCGGCGCCTTGGCCC 1424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: nisc_zoo@nhgri.nih.gov
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AC126232.1 GI:21693896
HTG; HTGS_PHASE1; HTGS_DRAFT.
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AC126232/c
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AUTHORS
TITLE
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ROD 29-JAN-2002

linear sequence.

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OK 73019, USA
3 (bases 1 to 209733)
Pan, H. and Roe, B.A.
Direct Submitted (08-NOV-2000) Department Of Chemistry And Biochemistry,
The University of Oklahoma, 620 Parrington Oval, Room 208, Norman,
                                                                                                                                                                                                                                                                                                                                                Submitted (19-APR-2000) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (29-JAN-2002) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
                                                                                                                                                                                                       Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
65094 GCCCTGGGGGCTACCGGCCCGACCGCTGCACCTTGCAGCTCTTCCCTTGTTATCCCCATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   495 CTCAGACAAAGAAGAGCTGGTGGGCGCGGAGCTGCGGCGCTCTTTCGCCAGGCGCCCTCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCCCTGGGGGCCACCAGCCGGGCCGCTCCACGTGCAGCTCTTCCCTTTCGCCCCT
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On Nov 8, 2000 this sequence version replaced gi:11119463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 765.8; DB 10
Pred. No. 1.2e-111;
                                                                                    209733 bp DNA
Mus musculus clone rp23-11707, complete
AC058786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44340 g 58095
                                                                                                                                                                                                                                                            Mus musculus BAC Clone rp23-11707
Unpublished
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/clone="rpp3-1170"
/clone=11b="RP2"
61917 a 45381 c 44340 g 58
                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
1 (bases 1 to 209733)
Pan,H. and Roe,B.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                          AC058786.23 GI:11120825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OK 73019, USA 4 (bases 1 to 209733) Pan, H. and Roe, B.A. Direct Submission
                                                                                                                                                                                                                                                                                                  2 (bases 1 to 209733)
Pan, H. and Roe, B.A.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 53.7%;
Best Local Similarity 87.4%;
Matches 866; Conservative
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                                                                                                                                                                         Mus musculus.
Mus musculus
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                                                                                                           DEFINITION
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                                                                                                                                                                                      CTCAGACAAAGAAGAGCTGGTGGGCGCGGGGCTGCGGCTTTTCGCCAGGCGCCCTCAGC
                                                                                                                                                                                                                                                    GCCCTGGGGGCCACCAGCCGGCCGCTCCACGTGCAGCTCTTCCCTTTCGCCCTTTCGCCCCT
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                1112 others
                                                                                            Indels
                                                          Score 798.8; DB 2;
Pred. No. 7.7e-117;
0; Mismatches 77;
                ų
                                                                                            0; Mismatches
             59765
/note="assembly_fragment"
49896 c 49290 g 59765
                                                          Query Match 56.1%;
Best Local Similarity 89.7%;
Matches 913; Conservative
                α
             59915
              COUNT
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Assembly program: XGAP4, version 4.5
Chemistry: Dye-terminator: 100% of reads
Consensus quality: 32085 bases at least Q40
Consensus quality: 321247 bases at least Q30
Consensus quality: 324562 bases at least Q20
Insert size: 325340; sum-of-contigs
Insert size: 175863; 3.3% error; agarose-fp
Quality coverage: 5.99% in Q20 bases; sum-of-contigs Quality
coverage: 11.18% in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                            * NOTE: This is a 'working draft' sequence. It currently consists of 13 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the fihished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              182459 273966 : config of 91508 bp in length 273967 274068 283037: contig of 9970 bp in length 274068 283037: contig of 9970 bp in length 283138 292484 292583: contig of 9970 bp in length 292584 292584: contig of 9946 bp in length 292584 295787: contig of 9970 bp in length 295788: contig of 9970 bp in length 295788: contig of 6997 bp in length 302885 302984: gap of 100 bp in length 302885 302986: contig of 18386 bp in length 100 bp
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15979 1678: gap of 100 bp
16079 48171: contig of 32639 bp in length
48718 48817: gap of 100 bp
92125 9224: gap of 100 bp
9225 127311: contig of 43307 bp in length
127312 127411: gap of 100 bp
127312 127411: gap of 100 bp
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159392 182357: contig of 22966 bp in length
182358 182458: gap of 101 bp
182459 273966: contig of 91508 bp in length
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1. .15978
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fragment_chain:1"
16079. .48717
/note="assembly_fragment:03208
fragment_chain:1"
48818 .92124
/note="assembly_fragment:03208
fragment_chain:1"
fragment_chain:1"
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                               site: http://www.sanger.ac.uk
                                                                                                                            Statistics
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/db_xref="taxon:10090"
/chromosome="4"
                                                                                                 Center project name: bM131A6
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                                                                                                                            ---- Summary
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Mus musculus chromosome 4 clone RP23-131A6, *** SEQUENCING IN
PROGRESS ***, 13 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 326540)
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64567
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AL732476.4 GI:21615719
HTG; HTGS_PHASE1; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP.
                                                                                                                                                              795 GCCGCCCCCGGACCTGCGGAGTCTGGGCTGCGGAGGGTGCGGCCTCCCCAGGAGCG
                                                                                                                                                                                                                                                            GGCCCTGCTGGTGGTATTCACCAGATCCCAGCGCAAGAACCTGTTCGCAGAGATGCGCGA
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31919

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Akhter, N., Antonellis, A., Ayele, K., Beckstrom-Sternberg, S.M.,
Benjamin, B., Blakesley, R.W., Bouffard, G.C., Breen, K., Brinkley, C.,
Benjamin, B., Blakesley, R.W., Euffard, G.C., Breen, K., Brinkley, C.,
Benjamin, P., Dietrich, N.L., Granite, S., Guan, X., Gupta, J.,
Haghighi, P., Hansen, N., Ho, S.-L., Idol, J.R., Karlins, E., Laric, P.,
Lee-Lin, S.-Q., Legaspi, R., Maduro, C.L., Maduro, V.B.,
Margulies, E.H., Masiello, C., Maskeri, B.,
McCloskey, J.C., McDowello, T., Pagulrigan, C., Pearson, R.,
Portnoy, M.E., Prasad, A., Schueler, M.G., Stantripop, S., Thomas, J.W.,
Thomas, P.J., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A.,
Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                     Sequencing Center, 8717
31800 TGAGCCCACTAACCATGCCATCATCAGACGCTGATGAACTCCATGGACCCGGGCTCCAC
                                                                                                                                              11860 CCCGCCTAGCTGCGTTCCCACCAAACTGACTCCCATTAGCATCCTGTACATCGACGC
                                                                                                                            CCCGCCCAGCTGCTGCGTGCCCACCAATTGACTCCCATCAGCATTCTATACATCGACGC
                                                                                                                                                                                                 GGGCAATAATGTGGTCTACAAGCAGTACGAGGACATGGTGGTGGAGTCGTGCGGCTGCAG
                                                      GGAGCCCACCAACCACGCCATCATCCAGACGCTGATGAACTCCATGGACCCCGGCTCCAC
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Submitted (03-APR-2002) NIH Intramural Seg
Grovemont Circle, Gaithersburg, MD 20877,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center: NIH Intramural Sequencing
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HTG; HTGS_PHASE1; HTGS_DRAFT.
Rattus norvegicus.
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DEFINITION
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SOURCE
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                                                               /note="assembly_fragment:00350"
274067 .283037_
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283138 .292483 .fragment:02119"
292584 .295787
/note="assembly_fragment:02168"
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321471..335540
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. 65929 c 68488 g 97422 t 1
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HTG 03-APR-2002

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1 (bases 1 to 1046)
Celeste, A.J., Wozney, J.M., Rosen, V.A., Wolfman, N.M., Thomsen, G.H. and Melton, D.A.
Methods of inducting formation of tendon and/or ligament tissue comprising administering BMP-12, BMP-13, and/or MP-52
Patent: US 5658882-A 31 19-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                          --GCCGGAGCCGAGGGGTCATGGCCAGC 76720
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                                                                                              1035 CACGGCCTTCGCCAGTCGCCATGGCAAGCGGCACGGCAAGAAGTCCAGGCTACGCTGCAG
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                                                                                                                                                                                                                                                                                                    CCCGCCCAGCTGCTGCGTGCCCACCAAATTGACTCCCATCAGCATTCTATACATCGACGC
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                                    Length 1046;
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les 84;
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Pred. No. 2.8e-
1; Mismatches
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314 c 331 g
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    76673 GCAGCTGGCTCTGCAGAGGCT--
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ilarity 87.2%;
Conservative
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KEYWORDS
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is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    301 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 52.6%; Score 749.8; DB 2; Best Local Similarity 86.4%; Pred. No. 4.2e-109; Matches 856; Conservative 0; Mismatches 122;
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/organism="Rattus norvegicus"

/strain="Brown Norway"

/db_xref="taxon:10116"

/clone="RP31-496H14"

/clone=lib="RP31"
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91313. .167312
/nocte="assembly_fragment"
a 35040 c 36627 g 47981
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/note="assembly_fragment
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vector_side:right"
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PAT 07-0CT-1997

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Search completed: November 25, 2002, 02:33:35 Job time : 5118 secs Appli Appli Appli Appli Appli Appli Appli Appli Appl

Sequence 2 Sequence 2 Sequence 2 Sequence 1 Sequence 1 Sequence 2 Sequence 2 Sequence 9 Sequence 9 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 1

Sequence 1 Sequence 2 Sequence 2 Sequence 2 Sequence 2

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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Celeste, Anthony J.
APPLICANT: Wozney, John
APPLICANT: Wozney, John
APPLICANT: Wolfman, Neil
APPLICANT: Thomsen, Gerald H.
APPLICANT: Thomsen, Gerald H.
APPLICANT: Thomsen, Gerald H.
APPLICANT: MILION, DOUGLAS A.
TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENETICS INSTITUTE, INC.
STRRET: ABOUT A COMPOSITIONS
CITY: Cambridge
STRRET: Massachusette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: MGSCULLE.
COUNTRY: USA
ZIP: 0140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBW PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/362,670B
FILING DATE: December 22, 1994
CLASSIFICATION: S14
ATORNEY/AGENT INFORMATION:
NAME: LAZAR, STEVEN R.
REGISTRATION NUMBER: 32,618
PURPER PROCKET NUMBER: 5202-D
                             US-08-808-324-29
PCT-US94-14030A-29
US-08-362-14030A-1
US-08-808-33-576C-1
US-08-808-324-1
US-08-808-324-1
US-08-414030A-1
US-08-455-559-9
US-09-145-060-9
US-08-33-576C-12
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; Patent No. 5658882
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 498-8260
TELEFAX: 617 876-5851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA (genomic)
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TYPE: nucleic acid
STRANDEDNESS: single
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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NAME/KEY: CDS
LOCATION: 2..964
FEATURE:
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US-08-362-670B-25
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/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
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Compugen Ltd.
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US-08-32-670B-31
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US-08-581-529B-5
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US-08-362-670B-33
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Copyright (c) 1993 - 2002
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Listing first 45 summaries
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Pred. No. 2.7e-185;
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Matches 987; Conservative
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US-08-362-670B-25
LOCATION:
                         Query Match
Best Local
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                                                              GENERAL INFORMATION:
APPLICANT: Celeste, Anthony J.
APPLICANT: Worney, John
APPLICANT: Wolfman, Neil
APPLICANT: Wolfman, Neil
APPLICANT: Welton, Douglas A.
ITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS
NUMBER OF SEQUENCES: ADDRESS:
ADDRESSEE: GENETICS INSTITUTE, INC.
                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC COMPALIBLE
OPERATORS: TSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/333,576C
FILING DATE: No. 6027919ember 2, 1994
CLASSIFICATION: 435
ATTORNEY,AGENT INFORMATION:
NAME: LAZAR, Steven R.
REGISTRATION NUMBER: 32,618
                                 Sequence 25, Application US/08333576C Patent No. 6027919
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                                                                                                                                                                                                                                         E: GENETICS INSTITUTE,
87 CambridgePark Drive
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 498-8260
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1171 base pairs
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Best Local Similarity 100.
Matches 987; Conservative
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605..964
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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RESULT 2
US-08-333-576C-25
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US-08-333-576C-25
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87 CambridgePark Drive
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Patent No. 6284872
GENERAL INFORMATION:
APPLICANT: Celeste, Anthony J.
APPLICANT: Rosen, Vicki A.
APPLICANT: Rosen, Vicki A.
APPLICANT: Wolfman, Neil
APPLICANT: Wolfman, Neil
APPLICANT: Melton, Douglas A.
TITLE OF INVENTION: TENDON-INDUCING
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
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US-08-808-324-25
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                                           COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FAPILCATION NUMBER: US/08/808,324
FILING DATE: Herewith
CLASSIFICATION: 514
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100.0%; Pred. No. 2.7e-185;
iive 0; Mismatches 0;
                                                                                                                                      CLASSIFICATION: 514
ATTORREY/AGENT INFORMATION:
NAME: Lazar, Steven
REGISTRATION NUMBER: 32,618
REFERENCE/DOCKET NUMBER: 5202
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 498-8260
TELEPHONE: 617 876-5851
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 1171 base pairs
TYPE: nucleic acid
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                                Floppy disk
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Best Local Similarity 100.
Matches 987; Conservative
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                COMPUTER READABLE FORM:
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TOPOLOGY: lin
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LOCATION:
FEATURE:
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US-08-808-324-25
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TELEFAX: 617 876-5851 INFORMATION FOR SEQ ID NO:
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GCCTTCGCCAGTCGCCATGGCAAGCGGCACGGCAAGAAGTCCAGGCTACGCTGCAGGAAG
                                                                                                    AAGCCCCTGCACGTGAACTTCAAGGAGCTGGGCTGGGACGACTGGATTATCGCGCCCCTG
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                                                                                                                                                                                                                                                                                                                                                           APPLICANT: GENETICS INSTITUTE, INC.
APPLICANT: PRESIDENT AND FELLOWS OF HARVARD COLLEGE
TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS
CORRESPONDENCE: 35
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Jecompatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin_Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                CGGTGCCTTTCCCGCCGCTTGGCCCG 1425
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R: 5202D-PCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: Massachusetts
CUNTRY: USA
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REGISTRATION NUMBER: 32,618
REFERENCE/DOCKET NUMBER: 52
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 498-8260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                   8 GATCTCTCGCACACTCCTCCGGAGACAATTTGTTTGATGATGTCCATGCTCTCA
                                                                                                                                                                                                                                                                                                                                                                                                68 GACAAAGAAGAGCTGGTGGGGGGGGGGGCTCTTTGGCGGGGCGCCTCAGGGCCC
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                                                                                                                                                                                                                                                        Length 1171;
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Pred. No. 2.7e-185;
                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                            69.3%; Scc.
100.0%; Pre
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                                                              TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                          IMMEDIATE SOURCE:
CLONE: Human VL-1 protein
                LENGTH: 1171 base pairs
                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                       NAME/KEY: mat_peptide
LOCATION: 605..964
SEQUENCE CHARACTERISTICS
                                                 single
                             nucleic acid
                                                                                                                                         NAME/KEY: CDS
LOCATION: 2..964
                                                                                                                                                                                                                                                                     Local Similarity
                                             STRANDEDNESS:
                                                                                                                                                                                                                        PCT-US94-14030A-25
                                                                                                                                                                                                                                                                                     Matches 987;
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952 GGGGCCGAGGGGTCGTGGCCGCCGCCGTCGGGCGCCCCGGATGCCAGGCCTTGGCTGCC 1011
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                                                                                         CGCCGGCCGGCTGGGAAGTC-TTCGACGTGTGGCAGGGCCTGCGCCCACCAGCCCTGGAAG
                                                                                                                                        CGCGCGCGGGGACCCCAGCAACCGCCCCCGGACCTGCGGAGTCTGGGCTTCGCCCGG
                                                                                                                                                                        1012 TCGCCCGGCCGCCGCGGCGCGCCACGCCTTCGCCAGTCGCCATGGCAAGCGGCACGGC
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                                                                        CAGCTGTGCTTGGAGCTGCGGGCCGCATGGGGCGAGCTGGACGCCGGGGAGGCCGAGGCG
                                                                                                                                                                                                         832 AGGGTGCGGCCTCCCCAGGAGCGGGCCCTGCTGGTGGTATTCACCAGATCCCAGCGCAAG
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APPLICANT: Wolfman, Neil II.
APPLICANT: Wolfman, Neil II.
APPLICANT: Melton, Douglas A.
APPLICANT: Melton, Douglas A.
APPLICANT: Melton, TENDON-INDUCING COMPOSITIONS
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 31, Application US/08333576C Patent No. 6027919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: GENETICS INSTITUTE, STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Celeste, Anthony J. APPLICANT: Wozney, John APPLICANT: Rosen, Vicki A.
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STATE: Massachusetts
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                                                                                                                                       AATAATGTGGTCTACAAGCAGTACGAGGACATGGTGGTGGTGGAGTCGTGCGGCTGCAGGTAG 1398
                                                                                                                                                       CCCAGCTGCTGCGTGCCCACCAAATTGACTCCCATCAGCATTCTATACATCGACGCGGGC
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                                                                                                                                                                                                                                                                                                                 Sequence 31, Application US/08362670B
Petent No. 5558882
GENERAL INFORMATION:
APPLICANT: Celeste, Anthony J.
APPLICANT: Wozney, John
APPLICANT: Wolfman, Vicki A.
APPLICANT: Thomsen, Gerald H.
APPLICANT: Thomsen, Gerald H.
APPLICANT: Thomsen, Gerald H.
APPLICANT: Thomsen, Tendon-Inducing Compositions
ITILE OF INVENTION: TENDON-INDUCING COMPOSITIONS
NUMBER OF SEQUENCES: 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/362,670B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40.8%; Score 581.8; DB 1;
87.2%; Pred. No. 7.4e-106;
live 1; Mismatches 84;
                                                                                                                                                                                                        CGGTGCCTTTCCCGCCGCTTGGCCCG 1425
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CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Lazar, Steven R.
REGISTRATION NUMBER: 32,618
REFREENCE/DOCKET NUMBER: 5202
TELECHMUNICATION INFORMATION:
TELEPHONE: 617 876-5851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 31: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 1046 base pairs
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Matches 675; Conservative
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EDNESS: single
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US-08-362-670B-31
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Best Local
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1192 GACTTCCCGCTGCGCTCGCACCTGGAGCCCACCAACCAGGCCATCATCCAGACGCTGATG 1251
                                                                                                              647 AACTCCATGGACCCGGGCTCCACCCCGCCTAGCTGCGTTCCCAAACTGACTCCC 706
                                                                                                                                                                           Gaps
                                                                        1252 AACTCCATGGACCCGGCTCCACCCGCCCAGCTGCTGCTGCTGCCCAAATTGACTCCC
                    1312 ATCAGCATTCTATACATCGACGCGGGCAATAATGTGGTCTACAAGCAGTACGAGGACATG
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                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Celeste, Anthony J.
APPLICANT: Wozney, John
APPLICANT: Rosen, Vicki A.
APPLICANT: Molfman, Neil
APPLICANT: Thomsen, Gerald A.
APPLICANT: Thomsen, Gerald A.
TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/808,324
FILING DATE: Herewith
CLASSIFICATION: 514
ATTORNEY/AGENT INPORMATION:
NAME: Lazar, Steven R.
REGISTRATION NUMBER: 32,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 40.8%; Score 581.8; DB 4;
Best Local Similarity 87.2%; Pred. No. 7.4e-106;
Matches 675; Conservative 1; Mismatches 84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3: GENETICS INSTITUTE, INC. 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                 Sequence 31, Application US/08808324 Patent No. 6284872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 520;
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 498-8260
TELEFAX: 617 876-5851
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 1046 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nucleic acid
EDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: Massachusetts
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STRANDEDNESS:
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US-08-808-324-31
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US-08-808-324-31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 653 GGCGGCCGGCTGGGAAGTC-TTCGACGTGTGGCAGGGCCTGCGCCACCACCCTGGAAG 711
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                                                                                CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/33,576C
FILING DATE: No. 6027919ember 2, 1994
CLASSIFICATION: 435
ATTORNEY/AGENT INPORMATION:
NAME: Lazar, Steven 82,618
REGISTRATION NUMBER: 32,618
REGISTRATION NUMBER: 5202-B
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1896-8260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 40.8%; Score 581.8; DB 3; Best Local Similarity 87.2%; Pred. No. 7.4e-106; Matches 675; Conservative 1; Mismatches 84;
                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                        TELEFAX: 617 876-5851
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                            LENGTH: 1046 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MURINE MV2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : LOCATION: 2..790
US-08-333-576C-31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 581.8; DB 5;
Pred. No. 7.4e-106;
1; Mismatches 84;
                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/164,103
FILING DATE: 07-DEC-1993
APPLICATION NUMBER: US 08/217,780
FILING DATE: 25-MAR-1994
APPLICATION NUMBER: US 08/333,576
FILING DATE: 02-NOV-1994
ATTORNEY/AGENT INFORMATION:
 APPLICATION DATA:
CATION NUMBER: PCT/US94/14030A
G DATE: Herewith
                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 5202D-PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 498-8260
TELEFAX: 617 876-5851
                                                                                                                                                                                                                             32,618
                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: DNA (genomic)
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87.2%;
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                                                                                                                                                                                                           NAME: Lazar, Steven R. REGISTRATION NUMBER: 33
                                                                                                                                                                                                                                                                                          TELEFAX: 617 876-5851
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 40.8°
Best Local Similarity 87.2°
Matches 675; Conservative
                                                                                                                                                                                                                                                                                                                                                                                    single
                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLONE: MURINE MV2
                                                                                                                                                                                                                                                                                                                                                                                                      linear
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                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANTI-SENSE: NO IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; NAME/KEY: CDS
; LOCATION: 2...
PCT-US94-14030A-31
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TOPOLOGY: lin
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                                                                                    CGCCGGCCGGCTGGAAGTC-TTCGACGTGTGGCAGGGCCTGCGCCACCACCACCTGGAAG
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                                 59 CCCAGGCCGGCTGGGAAGTCTTTCGACGTGTGGCAGGGCCTGCGCCCTCAGCCTTGGAAG
                                                                                                                                      CGCGCGCGCGCGCCCCCCCCCCCCCCCGGACCTGCGGAGTCTGGGCCTTCGGCCGG
                                                                                                                                                                                                        832 AGGGTGCGGCCTCCCCAGGAGCGGCCCTGCTGGTGGTATTCACCAGATCCCAGCGCAAG
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                                                                  CAGCTGTGCTTGGAGCTGCGGGCCGCATGGGGCGGAGCTGGACGCCGGGGAGGCCGAGGCG
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GENERAL INFORMATION:
APPLICANT: GENETICS INSTITUTE, INC.
APPLICANT: PRESIDENT AND FELLOWS OF HARVARD COLLEGE
TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSE: GENETICS INSTITUTE, INC.
STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 87 Cambrants CITY: Cambridge
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COUNTRY:
                                                                                                                                                                                                                                                                            892
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1156 CTGGAGTACGAGGCCTATCACTGCGAGGGTGTATGCGACTTCCCGCTGCGCTGCGCACCTG 1215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1276 CCGCCCAGCTGCTGCCCCACCAAATTGACTCCCCATCAGCATTCTATACATCGACGCG 1335
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61 CAGCTGGGCTCTGCAGAGGCT-------GCGGGAGCCGAGGGGTCATGGCCAGGG 108
                                                                                                            228 AGAAAGCCTCTGCACGTGAATTTTAAGGAGTAAGGCTGGGACGACGACTGGATTATCGCGCC 287
                                                                                                                                                                                                                                                                                                                                                                     168 ACCGCCTTCGCCAGCCGTCACGACAAGGACAAGAAGTAGAAATCCAGGCTGCGCTGCAGC
                                                                                                                                                           1036 ACGCCCTTCGCCAGTCGCCATGGCAAGCGGCAAGAAGTCCAGGCTACGCTGCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                          348 GAGCCCACTAACCATGCCATCATTCAGACGCTGATGAACTCCATGGACCCGGGCTCCACC
                                                                    CCGTCGGGCGCCCCGGATGCCAGGCCTTGGCTGCCCTCGCCCGGCCGCCGGCGGCGGCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 408 CCGCCTAGCTGCTGCGTTCCCACCAAACTGACTCCCATTAGCATCCTGTACATCGACGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Lee, Se-Jin
APPLICANT: Lee, Se-Jin
APPLICANT: Huynh, Thanh
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-6
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 4225 Executive Square, Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/097,616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07265/082001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 08/581,529 FILING DATE: 15-APR-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 5, Application US/09097616 Patent No. 6090563 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Lisa A. Haile, Ph.D. REGISTRATION NUMBER: 38,347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 07 TELECOMMUNICATION INFORMATION: TELEPHONE: (619) 678-5070 TELEPHONE: (619) 678-5099 INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: La Jolla
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
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US-09-097-616-5
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                     GACTTCCCGCTGCGCTCGCACCTGGAGCCCAACCAACCACGCCATCATCCAGACGCTGATG 1251
                                                                                                         1252 AACTCCATGGACCCCGGCTCCACCCCGCCCAGCTGCTGCGTGCCCACCAAATTGACTCCC 1311
                                                                                                                                      856 GCCCTGCTGGTGGTATTCACCAGATCCCAGCGCAAGAACCTGTTCGCAGAGATGCGCGAG 915
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                                                                                                                                                                                                                                                                                                                 Length 530;
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APPLICANT: Lee, Se-Jin
APPLICANT: Huynh, Thanh
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-6
TORRESPONDENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STRET: 4225 Executive Square, Suite 1400
CITY: La Johla
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE PATENTIN Release #10, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 15-APR.1996
CLASSIFICATION: 536
ATTONREY/AGENT INFORMATION:
NAME: Lisa A. Haile, Ph.D.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/082001
TELECOMMULICATION INFORMATION:
TELECOMMULICATION INFORMATION:
TELEFRAM: (619) 678-509
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 530 base pairs
TENETH 530 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 5, Application US/08581529B Patent No. 5770444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: DNA (genomic)
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; LOCATION: 126..527
US-08-581-529B-5
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                                                                                                                                         Length 530;
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GENERAL INFORMATION:
APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE TITLE OF INVERTION: GROWTH DIFFERENTIATION FACTOR-6
NUMBER OF SEQUENCES: 21
                                                                                                                                                              Indels
                                                                                                                                      Score 412.2; DB 3;
Pred. No. 1.2e-72;
0; Mismatches 53;
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1880 Century Park East, Suite 500
                                   TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
IMMEDIATE SOURCE:
CLONE: GDF-6
                                                                                                                                      Query Match 28.9%;
Best Local Similarity 87.8%;
Matches 477; Conservative (
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1: 530 base pairs
nucleic acid
EDNESS: single
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ADDRESSEE: Spensley
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126..527
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CITY: Los Angeles
STATE: California
COUNTRY: USA
             TYPE: nuclei
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                                                                                          NAME/KEY:
LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28.9%; Score 412.2; DB 5; 87.8%; Pred. No. 1.2e-72;
                                      Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
              OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/07762
                                                                                                        CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: TUMARKIN, LISA A; PH.D.
REGISTRATION NUMBER: P-38,347
REFERENCE/DOCKET NUMBER: F-2349
TELECOMMUNICATION INFORMATION:
TELEPRONE: (619) 455-5100
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: DNA (genomic) IMMEDIATE SOURCE:
                                                                                            08-JUL-1994
                                                                                                                                                                                                                                                                                                     LENGTH: 530 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                      linear
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                                                                                              FILING DATE:
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1135 ATGCCATCATTCAGACGCTGCTCAACTCCATGGCACCAGACGCGGCGCCGCCTCCTGCT 1194
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535 TGTACTCGCGGCCAGCTGAGCCCCTAGTCGGTCAGCGCTGGGAGGCGTTCGACGTGGCGG 594
                                           704 CCTGGAAGCAGCTGTGCTTGGAGCTGCGGGCCGCATGGGGCGAGCTGGACCCCGGGGAGG 763
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APPLICANT: Mozney, John
APPLICANT: Rosen, Vicki A.
APPLICANT: Molfman, Neil
APPLICANT: Thomsen, Gerald H.
APPLICANT: Melton, Douglas A.
TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 33, Application US/08333576C
; Patent No. 6027919
; GENERAL INFORMATION:
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87 CambridgePark Drive
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MEDIUM TYPE: Floppy disk
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CITY: Cambridge
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                                                                                                 APPLICANT: Celeste, Anthony J.
APPLICANT: Celeste, Anthony J.
APPLICANT: Mozney, John
APPLICANT: Molfman, Neil
APPLICANT: Thomsen, Gerald H.
APPLICANT: Thomsen, Gerald H.
APPLICANT: Melton, Douglas A.
TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENETICS INSTITUTE, INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/362,670B
FILING DATE: December 22, 1994
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 18.2%; Score 259.2; DB 1; Best Local Similarity 57.8%; Pred. No. 1.4e-42; Matches 550; Conservative 0; Mismatches 378;
                                                                                                                                                                                                                                                                                                             ADDRESSEE: GENETICS INSTITUTE, INC. STREET: 87 CambridgePark Drive CITY: Cambridge STATE: Massachusetts
COUNTRY: USA
                                      Sequence 33, Application US/08362670B
Patent No. 5658882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: LAZAT, Steven R.
REGISTRATION NUMBER: 52618
REFERENCE/DOCKET NUMBER: 5202
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 898-8260
TELEPHONE: 617 876-5851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 1345 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
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LOCATION: 990..1301
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LOCATION: 138..1301
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IMMEDIATE SOURCE:
CLONE: HUMAN VI-1
                                                                                  GENERAL INFORMATION:
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US-08-362-670B-33
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989 CGGATGCCAGGCCTTGGCTGCCCTCGCCGGCCGCGGCGGCGGCGCACGGCCTTCGCCA 1048
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 33, Application US/08808324 Patent No. 6284872 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 498-8260
TELEFAX: 617 876-5851
INFORMATION FOR SEQ ID NO: 33:
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NAME: Lazar, Steven R.
REGISTRATION NUMBER: 32,6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 1345 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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US-08-808-324-33
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 259.2; DB 3;
Pred. No. 1.4e-42;
0; Mismatches 378;
                                                                 APPLICATION NUMBER: US/08/333,576C
FILING DATE: No. 6027919ember 2, 1994
CELESSIFICATION: 435
ATTORREY/AGENT INFORMATION:
NAME: Lazar, Steven R.
REGISTRATION NUMBER: 32,618
REFERENCE/DOCKET NUMBER: 5202-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 498-8260
TELEPHONE: 617 498-8260
TELEPHONE: 617 498-8260
TELEPHONE: 1345-5851
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 1345 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 18.2%;
Best Local Similarity 57.8%;
Matches 550; Conservative
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990..1301
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138..1301
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IMMEDIATE SOURCE:
CLONE: HUMAN V1-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY:
LOCATION:
FEATURE:
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US-08-333-576C-33
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                                                       GTCGCCATGGCAAGCGGCACGGCAAGAAGTCCAGGCTACGCTGCAGCAAGAAGCCCCTGC
                                                                                                                                                                    ACGTGAACTTCAAGGAGCTGGGCTGGGACGACTGGATTATCGCGCCCCTGGAGTACGAGG
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895 GCGGCCGCAGACGGAGGACGCCTTGGCCGGGACGCGGACAGCGCAGGGCAGCGCG
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APPLICANT: Mozney, John
APPLICANT: Rosen, Vicki A.
APPLICANT: Rosen, Vicki A.
APPLICANT: Molfman, Neil
APPLICANT: Thomsen, Gerald H.
APPLICANT: Melton, Douglas A.
TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/808,324
FILING DATE: Herewith
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1195 GTGTGCCAGCGCGCCTCAGCCCCATCAGCATCTTACATCGACGCCGCCAACAACGTTG 1254
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                                  1349 TCTACAAGCAGTACGAGGACATGGTGGTGGAGTCGTGCGGCTGCAGGTAGCG 1400
                                                     1255 TCTACAAGCAATACGAGGACATGGTGGTGGAGGCCTGCGGCTGCAGGTAGCG 1306
                                                                                                                                                       Sequence 33, Application PC/TUS9414030A
GENERAL INFORMATION:
APPLICANT: GENETICS INSTITUTE, INC.
APPLICANT: PRESIDENT AND FELLOWS OF HARVARD COLLEGE
TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18.2%; Score 259.2; DB 5; 57.8%; Pred. No. 1.4e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches 378;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PALLOR TO DATE: US 08/164,103
FILING DATE: 07-DEC-1993
APPLICATION NUMBER: US 08/217,780
FILING DATE: 25-MAR-1994
APPLICATION NUMBER: US 08/33,576
FILING DATE: 02-NOV-1994
ATORNEY/AGENT INFORMATION:
NAME: LAZAR, STEVEN R.
REGISTRATION NUMBER: 32,618
REFERENCE/POCKET NUMBER: 5202D-PCT
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 498-8260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/14030A
FILING DATE: Herewith
CLASSIFICATION:
                                                                                                                                                                                                                                                                                   E: GENETICS INSTITUTE, INC. 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 33: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 1345 base pairs
TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                     STATE: Massachusetts
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Matches 550; Conserv
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                                                                                                                                                                                                                                                                                                                                                         USA
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                                                                                                                                          PCT-US94-14030A-33
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ANTI-SENSE:
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Pred. No. 1.4e-42;
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Best Local Similarity 57.8%;
Matches 550; Conservative (
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ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: HUMAN V
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COMPUTER READABLE FORM:
MEDIUM TYPE: FLORPY disk
MEDIUM TYPE: FLORPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRIT APPLICATION DATE:
FILING DATE: 31-Aug-2001
CLASSIFICATION: CURROWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wolfman, Neil
Thomsen, Gerald H.
Melton, Douglas A.
TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
                            US-09-784-911-11

US-09-784-911-11

US-09-784-911-13

US-09-766-397-1

US-08-927-248

US-08-937-755-1

US-08-937-755-1

US-09-982-543A-9

US-09-982-543A-9

US-09-982-543A-9

US-09-982-543A-9

US-09-982-6731-1

US-09-954-456-1824

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US-09-954-456-1824

US-09-765-327-256

US-09-765-327-256

US-09-765-327-254

US-09-768-911-7

US-09-784-911-9

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US-09-784-911-5
US-09-764-869-1535
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STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Lazar, Steven R.
REGISTRATION NUMBER: 32,618
REFERENCE,DOCKET NUMBER: 5202-D
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 498-8350
TELEFAX: 617 876-5851
INFORMATION FOR SEQ ID NO: 25:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
RAPLICATION NUMBER: 08/808,324
FILING DATE: <UNKnown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 25, Application US/09945182
Patent No. US20020166494A1
GENERAL INFORMATION:
APPLICANT: Celeste, Anthony J.
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Rosen, Vicki A.
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COUNTRY: USA
   SEQUENCE CHARACTERISTICS
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   Sequence 582, App
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/cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
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                            GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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US-09-945-182-1

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1279 CCCAGCTGCTGCTGCCCACCAAATTGACTCCCATCAGCATTCTATACATCGACGCGGGC 1338
                                                                                       AATAATGTGGTCTACAAGCAGTACGAGGACATGGTGGTGGAGTCGTGCGGCTGCAGGTAG 1398
                                                                                                      GGGCGCCGCGCGACAGTGACGCGGGCCGGGAG------GGCCAGGAACCACAGCCGC 238
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 CCCACCAACCACGCCATCATCCAGACGCTGATGAACTCCATGGACCCCGGCTCCACCCCG
                                              848 CCCAGCTGCTGCGTGCCCACCAAATTGACTCCCATCAGCATTCTATACATCGACGGGG
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                                                                                                                                                                                                                                                                                       APPLICANT: Luyten, Frank P.
APPLICANT: Luyten, Frank P.
APPLICANT: Moos, Jr., Malcolm
APPLICANT: Chang, Steven Chao-Huan
TITLE OF INVENTION: CARTILAGE-DERIVED MORPHOGENETIC
NUMBER OF SEQUENCES: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 928.2; DB 10;
Pred. No. 5e-180;
0; Mismatches 123;
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: 620 Newport Center Drive, 16th Floor
Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: FastSEQ for Windows Version 2.0b CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/730,772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NIH099.001APC
                                                                                                                                               CGGTGCCTTTCCCGCCGCCTTGGCCCG 1425
                                                                                                                                                              968 CGGTGCCTTTCCCGCCGCCTTGGCCCG 994
                                                                                                                                                                                                                                               Sequence 12, Application US/09730772 Patent No. US20010011131A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/836,081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Bartfeld, Neil S
REGISTRATION NUMBER: 39,901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: NI
TELECOMMUNICATION INFORMATION:
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86.5%;
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Matches 1136; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Diskette
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                                                                                                                                                                                                                                                                                                                                                   TGGGGGCCCACCAGGCCGCCTCCACGTGCAGCTCTTCCCTTGCCTTTCGCCCTACTG
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                                                                                                                                                                                                                    Length 1171;
                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                 69.3%; Score 987; DB 9; Lv
100.0%; Pred. No. 5.7e-192;
iive 0; Mismatches 0;
                                                                                                                                                           LOCATION: 605. 964
SEQUENCE DESCRIPTION: SEQ ID NO: 25:
                                                                   CLONE: Human VL-1 protein
             STRANDEDNESS; single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                            mat_peptide
605..964
TYPE: nucleic acid
                                                                                                                                                                                                                                Best Local Similarity 100.
Matches 987; Conservative
                                                       IMMEDIATE SOURCE:
                                                                                                   NAME/KEY:
                                                                                                                 LOCATION:
                                                                                                                                             NAME/KEY:
                                                                                                                             FEATURE
                                                                                                                                                                                      US-09-945-182-25
                                                                                    FEATURE
                                                                                                                                                                                                                   Query Match
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                 1283 GCTGCTGCGTGCCCACCAAATTGACTCCCATCAGCATTCTATACATCGACGCGGGCAATA 1342
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                                                                         1343 ATGTGGTCTACAAGCAGTACGAGGACATGGTGGTGGAGTCGTGCGGCTGCAGG 1395
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                                                                                                                                                                                                        Sequence 12, Application US/09735849
Patent No. US20010037017A1
GENERAL INFORMATION:
APPLICANT: Luyten, Frank P.
APPLICANT: Chang, Steven Chao-Huan
TITLE OF INVENTION: CRATILAGE-DERIVED MORPHOGENETIC
TITLE OF INVENTION: CRATILAGE-DERIVED MORPHOGENETIC
NUMBER OF SEQUENCES: 24
                                                                                                                                                                                                                                                                                                                                                     STREET: 620 Newport Center Drive, 16th Floor CITY: Newport Beach STATE: CAPOUTRY: U.S.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: Mindows SOFFWARE: FastSEQ for Windows Version 2.0b CURRENY APPLICATION DAFA: US/09/735,849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Barffeld, Nails
REGISTRATION NUMBER: 39,901
REFERENCE/DOCKET NUMBER: NIH099.001APC
TELECOMMUTCATION INFORMATION:
TELEPHONE: 619-235-8550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/836,081
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 1308 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 65.1
Best Local Similarity 86.5
Matches 1136; Conservative
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CLASSIFICATION:
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STRANDEDNESS:
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MOLECULE TYPE:
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US-09-735-849-12
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US-09-735-849-12
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                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                              Melton, Douglas A.
DF INVENTION: TENDON-INDUCING COMPOSITIONS OF SEQUENCES: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; DB 9;
.3e-110;
les 84;
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; Pred. No. 9.3e-
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/945,182
FILING DATE: 31-Aug-2001
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5202-D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31:
                                                                                                                                                                                                                                        ADDRESSEE: GENETICS INSTITUTE, STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/808,324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Lazar, Steven R.
REGISTRATION NUMBER: 32,618
REFERENCE/DOCKET NUMBER: 5202-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 496-8260
TELEFAX: 617 876-8851
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                     ; Sequence 31, Application US/09945182
; Patent No. US20020160494A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
                                                                                                                                                         Wolfman, Neil
Thomsen, Gerald H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 1046 base pairs
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                                                                                                                Anthony
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: <Unknown>
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                                                                                                                             Wozney, John
Rosen, Vicki A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                    STATE: Massachusetts
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                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
                                                                                                                                                                                              TITLE OF INVENTION: TEN
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLONE: MURINE MV2
                                                                                                                                                                                                                                                                    CITY: Cambridge
                                                                                                               APPLICANT: Celeste,
                                                                                                                                                                                                                                                                                               COUNTRY: USA
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                                            RESULT 4
US-09-945-182-31
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Best Local 9
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185 GCAGGGCCCCGCCTTGTGCCCCCACGAGTACATGCTGTCAATCTACAGGACTTACTCCA
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                                                                                                                                                                    CGCCGCCCGCCCGCTGGGAAGTCTTCGACGTGTGGCAGGGCCTGCGCCACCAGCCCTGGA
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                                                           832 AGGGTGCGGCCTCCCCAGGAGCGGGCCCTGCTGGTGGTATTCACCAGATCCCAGCGCAAG
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COMPUTER: IBM PC Compatible
SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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Rosen, Vicki A.
Wolfman, Neil
Thomsen, Gerald H.
Melton, Douglas A.
INVENTION: TENDON-INDUCING COMPOSITIONS
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APPLICATION NUMBER: US/09/945,182
FILING DATE: 31-Aug-2001
CLASSIFICATION: <unional content of the c
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Patent No. US20020160494A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Celeste, Anthony
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CORRESPONDENCE ADDRESS:
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COMPUTER READABLE FORM:
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US-09-945-182-33
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Pred. No. 2.8e-44;
0; Mismatches 378;
                                                          NAME: Lazar, Steven R.
REGISTRATION NUMBER: 32,618
REGISCATION LOWBER: 5202-D
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 498-8260
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 1345 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: mat_peptide
LOCATION: 990..1301
SEQUENCE DESCRIPTION: SEQ ID NO: 33:
APPLICATION NUMBER: 08/808,324
                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                     FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 57.8%;
Matches 550; Conservative
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                                                                                       2008 GACCCCCAGTCCACCACCACCACCTGCTGTGTGTCCCACCGGCTGAGTCCCATCAGCATC
                                                                  GACCCCGGCTCCACCCCGCCCAGCTGCTGCGTGCCCAAATTGACTCCCATCAGCATT
                                                                                                                                                   CTATACATCGACGCGGCAATAATGTGGTCTACAAGCAGTACGAGGACATGGTGGTGGTGGAG
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WEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/945,182
FILING DATE: 31-ANG-2001
CLASSIFICATION: <UNROWN>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Celeste, Anthony J.
Wozney, John
Rosen, Vicki A.
Wolfman, Neil
Thomsen, Gerald H.
Melton, Douglas A.
TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATORICATION NUMBER: 08/808,324
FILING DATE: CUNTROWNATION:
NAME: Lazar, Steven R.
REGISTRATION NUMBER: 32,618
REFERENCE/DOCKET NUMBER: 5202-D
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17.7%; Score 251.6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: 845.1204
SEQUENCE DESCRIPTION: SEQ ID
US-09-945-182-3
                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/09945182 Patent No. US20020160494A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 1207 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                   2128 TCGTGTGGCTGCAGGTAGCAG 2148
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                                                                                                                                                                                                                                  1381 TCGTGCGGCTGCAGGTAGCGG 1401
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INFORMATION FOR SEQ ID NO: 3:
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APPLICANT: Pohl, Jens
TITLE OF INVENTION: UNBLOKER, MICHAEL
TITLE OF INVENTION: UNBLOKER, MICHAEL
TITLE OF INVENTION: UNBLOKE, MICHAEL
FILE REFERENCE: 100564-07032
CURRENT APPLICATION NUMBER: US/08/981,490B
FILE REFERENCE: 1096-07-12
PRIOR APPLICATION NUMBER: DCT/EP96/03065
PRIOR APPLICATION NUMBER: DCT/EP96/03065
PRIOR APPLICATION NUMBER: DCT/EP96/03065
PRIOR APPLICATION NUMBER: DCT/EP96/03065
PRIOR PILING DATE: 1996-07-12
PRIOR FILING DATE: 1995-07-12
NUMBER OF SEQ ID NOS: 7
SOOFWARE: PatentIn version 3.1
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                                                                                                        1015 ACGTGGACTTCAAGGAGCTCGGCTGGACGACTGGATCATCGCGCGCTGGACTACGAGG 1074
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1049 GTCGCCATGGCAAGCGGCAACGCAAGAAGTCCAGGCTACGCTGCAGCAAGAAGCCCCTGC
                                        955 GGGCGCGGGCCGGGGCCACGGGCCAGGGGCCGGAGCCGCTGCAGCCGCAAGCCGTTGC
                                                                                                                                                                                          ACGCCATCATCCAGACGCTGATGAACTCCATGGACCCCGGCTCCACCCGGCCCAGCTGCT
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Matches 301; Conservative
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OTHER INFORMATION:
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ORGANISM: Homo sapiens
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NAME/KEY: CDS
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LENGTH: 2703
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1021 CGCCGGCGGCGCGCACGGCCTTCGCCAGTCGCCATGGCAAGCGGCACGGCAAGAAGTCC 1080
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                                                                                                                         Length 2341;
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                                                                                                                                                            81; Indels
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                                                                                                                       Score 251.4; DB 10;
Pred. No. 1.2e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive, 16th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: Windows
SOFTWARE: FESTENG for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/735,849
                                                                                                                                                            0; Mismatches
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ATTORNEY/AGENT INFORMATION:
NAME: Bartfeld, Neil S
REGISTRATION NUMBER: 39,901
REFERENCE/DOCKET NUMBER: NIH099.001APC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Luyten, Frank P.
APPLICANT: MOOS, Jr., Malcolm
APPLICANT: Chang, Steven Chao-Huan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 11, Application US/09735849
Patent No. US20010037017A1
GENERAL INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/836,081
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                                                                                                                       17.6%;
78.7%;
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COMPUTER: IBM Compatible
                                                                                                                                                            Matches 300; Conservative
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CORRESPONDENCE ADDRESS:
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ZIP: 92660
COMPUTER READABLE FORM:
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           nucleic acid
                         ; STRANDEDNESS: SII;
; TOPOLOGY: linear
; MOLECULE TYPE: CDNI
US-09-730-772-11
                                                                                                                                          Best Local Similarity
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                           Indels
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Patent No. US20010011131A1
GENERAL INFORMATION:
APPLICANT: LUYEN, Frank P.
APPLICANT: Chang, Steven Chao-Huan
APPLICANT: Chang, Steven Chao-Huan
TITLE OF INVENTION: CARTILAGE-DERIVED MORPHOGENETIC
TITLE OF INVENTION: PROTEINS
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
No. 9.6e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUFTWARE: FRACESED for Windows CURRENT APPLICATION DATA: WINDOWS APPLICATION NUMBER: US/09/730,772 FILING DATE: CLASSIFICATION:
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620 Newport Center Drive, 16th Floor
                       0; Mismatches
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         Pred.
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APPLICATION NUMBER: 08/836,081
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: BATFFELD, Neil S
REGISTRATION NUMBER: 39,901
REFERENCE/DOCKET NUMBER: NII
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-235-8550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 11:
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       79.18;
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                         Conservative
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MEDIUM TYPE: Diskett
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STATE: CA
       Similarity
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     Local Simines 299;
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US-09-730-772-11
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                                                                                                                                                                                                                                    DB 10; Length 2341;
                                                                                                                                                                                                                                                                   Indels
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APPLICANT: HIROYUKI; MIKI, HIDEO; KAWAI,
APPLICANT: SHINJI; KIMURA, MICHO; MATSUMOTO,
APPLICANT: TOMOAKI; KATSUURA, MIEKO; ENOMOTO,
APPLICANT: KOICHI; SATOH, YUSUKE
TITLE OF INVENTION: A NOVEL PROTEIN AND
TITLE OF INVENTION: PROCESS FOR PREPARING THE SAME
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                               Score 251.4; DB 10;
Pred. No. 1.2e-42;
0; Mismatches 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: BIERMAN, MUSERLIAN AND LUCAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: MICROSOFT WORD 97
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IBM PC COMPATIBLE
TELECOMMUNICATION INFORMATION:
                                                                    INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                               17.6%;
78.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: LLP
STREET: 600 THIRD AVENUE
CITY: NEW YORK
                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 2341 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                TELEPHONE: 619-235-8550
TELEFAX: 619-235-0176
                                                                                                                                                                                                                               Query Match 17.6's
Best Local Similarity 78.7's
Matches 300; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: FLOPPY |
                                                                                                                                                          TOPOLOGY: ilnear MOLECULE TYPE: CDNA US-09-735-849-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10016
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                                                     TELEX:
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1043 TCGCCAGTCGCCATGGCAAGCGGCACGCCAAGAAGTCCAGGCTACGCTGCAGCAAGAAGC 1102
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Patent No. US20020168381A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL SHIMURA, TAKESADA
APPLICANT: SHIMURA, TAKESADA
APPLICANT: TORIYAMA, SALSUKİ
TITLE OF INVENTION: CARTILAGE/ BONE INDUCING MATERIALS FOR REPARATION
FILE OF INVENTION:
GURRENT APPLICATION NUMBER: US/09/068,253
CURRENT FILING DATE: 1998-06-09
PRIOR FILING DATE: 1996-11-17
PRIOR FILING DATE: 1996-11-17
PRIOR FILING DATE: 1996-11-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1103 CCCTGCACGTGAACTTCAAGGAGCTGGGCTGGGACGACTGGATTATCGCGCCCCTGGAGT
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Pred. No. 1.2e-41;
0; Mismatches 67;
APPLICATION NUMBER: US/08/945,459A FILING DATE: 09-DEC-1997
PRIOR APPLICATION DATA: APPLICATION NUMBER: PCT/JP96/01062
FILING DATE: 19-APR-1996
                                                                                                                                                                                                                                                                                                                                                    146.1275
                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP7/322403
FTLING DATE: 17-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP7/93664
FTLING DATE: 19-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: CHARLES A MUSERLIAN
REGISTRATION NUMBER: 19,683
                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION
TELEPHONE: (212) 661-8000
TELEFAX: (212) 661-8002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17.2%;
81.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 357 BASE PAIRS
NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 81.0
Matches 286; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
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US-08-945-459A-4
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US-09-068-253-1
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SOFTWARE: Patentin Release #1.0, Version #1.25
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US-09-945-182-1
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Best Local (
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                                                                                                             amino acid residues in SEQ ID NO: 1 from in WO 95/04819
                                                                                                                                                                                                                                                                                                                                                                                                       245 CCTGCTGTGTGCCCACGGACTGAGTCCCATCAGTCTCTTCATTGACTCTGCCAACA
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                                                                                         LOCATION: (1)..(357)
COTHER INFORMATION: Relevant amino acid residues in SEQ ID NO OTHER INFORMATION: 1 to 119 in WO 95/04819
O'THER INFORMATION: 1 to 119 in WO 95/04819
PUBLICATION INFORMATION:
AUTHORS: HEDHARATION:
AUTHORS: PALLISTRA, Michael
TITLE: PAMILY
PATENT DOCUMENT NUMBER: WO 95/04819
PATENT DOCUMENT NUMBER: WO 95/04819
PATENT PILING DATE: 1995-02-16
PATENT FILING DATE: 1995-02-16
                                                                                                                                                                                                                                                                                                                                                       Indels
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TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                        DB 9;
                                                                                                                                                                                                                                                                                                                    Query Match 17.2%; Score 245.8; DB 9
Best Local Similarity 81.0%; Pred. No. 1.2e-41;
Matches 286; Conservative 0; Mismatches 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: GENETICS INSTITUTE, INC. STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 29, Application US/09945182
Patent No. US/0010160494A1
GENERAL INFORMATION:
Mozney, John
Rosen, Vicki A.
Wolfman, Neil
Thomsen, Gerald H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Cambridge
                                              ORGANISM: Homo sapiens
                                                                              NAME/KEY: CDS
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US-09-945-182-29
SEQ ID NO 1
LENGTH: 357
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                                 TYPE: DNA
                                                                FEATURE
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1087 CGCTGCAGCAAGAAGCCCCTGCACGTGAACTTCAAGGAGCTGGGCTGGGACGACTGGATT 1146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GC-CGCCGTCGGGCGCCCCGGATGCCAGGCCTTGGCTGCCCTCGCCCGGCCGCCGGCGGCGC
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ilarity 71.2%; Pred. No. 2.1e-41;
Conservative 0; Mismatches 137;
                                                                                              PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/808,324

TILING DATE: CURKNOWN-
ATTORNEY/AGENT INFORMATION:

NAME: Lazar, Steven R.

REGIGSTRATTON NUMBER: 32,618

REFERENCE/DOCKET NUMBER: 5202-D

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617 498-8260

TELEPRA: 617 876-5851

INFORMATION FOR SEQ ID NO: 29:

SEQUENCE CHARACTERISTICS:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: U$/09/945,182
FILING DATE: 31-Aug-2001
CLASSIFICATION: CURKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: 2..721
SEQUENCE DESCRIPTION: SEQ ID NO: 29
                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 1203 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
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NAME: Lisa A. Haile, Ph.D. REGISTRATION NUMBER: 38,347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: 858/677-1456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 9, Application US/09880708
Patent No. US20020165361A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 92121-2189
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 619/677-1465 INFORMATION FOR SEQ ID NO: 9:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: San Diego
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-880-708-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      294 GCCGGGCGGAGGGGCTCTGCGGCAGAGCGCGCGGGGGGTAGTCGTCTCCTCCCGCAC 353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 926;
                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIAN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/945,182
FILING DATE: 31-Aug-2001
CLASSIFICATION CURROWN>
PRIOR APPLICATION DATA:
                                                                                       Wolfman, Neil
Thomsen, Gerald H.
Melton, Douglas A.
FINTENTION: TENDON-INDUCING COMPOSITIONS
OF SEQUENCES: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 17.2%; Score 244.8; DB 9; Best Local Similarity 64.7%; Pred. No. 2.2e-41; Matches 423; Conservative 0; Mismatches 207;
                                                                                                                                                                                  ADDRESSEE: GENETICS INSTITUTE, INC. STREET: 87 CambridgePark Drive CITY: Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 08/808,324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: 1..882
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                         ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
Sequence 1, Application US/09945182
Patent No. US2002016160494A1
GENERAL INFORMATION:
APPLICANT: Celeste, Anthony
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 926 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens IMMEDIATE SOURCE:
                                                                         Rosen, Vicki A.
                                                                                                                                                                                                                                STATE: Massachusetts
COUNTRY: USA
                                                              Wozney, John
                                                                                                                                   TITLE OF INVENTION: TEN
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .882
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                                                                                         833
414 TCTGGCCTCAGAGCCGCTGCCCGACCCAGGAACCGGCACCGCGTCGCCAAGGGCAAGTCAT 473
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TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version 2.0
CURRIT APPLICATION DATA:
APPLICATION NUMBER: US/09/880,708
FILING DATE: 12-Jun-2001
PRIOR APPLICATION NUMBER: 09/145,060
FILING DATE: CUNKNOWND
APPLICATION NUMBER: 09/145,444
FILING DATE: CUNKNOWND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Gray Cary Ware & Freidenrich LLP
STREET: 4365 Executive Drive, Suite 1600
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TITLE OF INVENTION: No. US20020132090Alel Nucleic Acid and Protein Homologs
TITLE OF INVENTION: No. US20020132090Alel Nucleic Acid and Protein Homologs
CURRENT APPLICATION NUMBER: US/09/833,381
CURRENT FILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: 09/516,448
PRIOR FILING DATE: 2000-02-29
                                                                                                                                                                                                                                                                                                                                                                                                                                          1021 CGCCGGCGGCGCGCACGCCCTTCGCCAGTCGCCATGGCAAGCGGCACGCCAAGAAGTCC 1080
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Best Local Similarity 74.9%; Pred. No. 3.8e-40;
Matches 299; Conservative 0; Mismatches 100; Indels
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 582
LENGTH: 475
                                                                                                            NAME/KEY: Coding Sequence
LOCATION: 322...1806
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 582, Application US/09833381
Patent No. US20020132090A1
GENERAL INFORMATION:
                  TOPOLOGY: linear MOLECULE TYPE: Genomic DNA
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Homo sapiens US-09-833-381-582
                                                      IMMEDIATE SOURCE:
CLONE: GD-5
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US-09-833-381-582
                                                                                            FEATURE
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68 GGGCGGGGCGAGGGCCGGAGCCGCTGCAGCCGTTGCACGTGGA 127
                              GCAGTACGAGGACATGGTGGTGGAGTCGTGCGGCTGCAGGTAGCG 1400
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GenCore version
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Human full length Murine mV2 protein Murine BMP-13 homo Murine partial mV2

bone morphog full length

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AAW36100 AAW19210 AAW11900	AAW01799 AAW12770 AAW44868	AAM33008 AAR60023 AAB84550	AAR95635 AAY92034	AAB70529	AAW26597 AAE10986	AAB12986	AAR78729 AAW26589	AAE10973 AAM51933	AAW26597 AAE1098	AAR78738 AAW26594	AAE10984 ABG2937	AAB09554	AAY92579 AAB09555 AAB02821	ALIGNMENT	455 AA.			factor-6	ntiation fac .oma; glioma;			Signal_peptid Mature_protei						Fernandes E
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CAMF10 is expressed in astrocytoma and glinoma-derived tissue. DNA encoding the AMF8 may be useful in gene therapy, and the protein cancer and other cell proliferative disorders. Generally, the cancer and other cell proliferative disorders. Generally, the cather of calmad other caids and proteins of the invention are useful for treating or preventing AMFX-associated disorders, e.g. a disorder related to cell signal processing and metabolic pathway modulation, chances triangly in trophic factor limited secondary tissue site microenvironments, connective tissue disorders tissue remodeling oncogenesis, connective tissue covary, cervix, prostate, endometrium, stomach, colon, lung, blandder, kidney, brain, and soft-tissue, cellular transformation, chantion and resorption, haematopoiesis, anglogenesis, multidrug resistance related to organic anion transporters, malignant disease cellular responses to external stimuli, and other diseases. Consecting and paractine requisition of cell growth, and cellular responses to external stimuli, and other diseases.
                                                                                                                                             New AMF1-10 polypeptides and encoding polynucleotides, useful for treating or preventing disorders related to modulation of cell movement, cell signal processing, cell adhesion or migration pathways
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GREGGEPQPRPQDEPRAQOPRAQEPPGRGPRVVPHEYMLSIYRTYSIAEKLGINASFFQS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DAGEAEARARGPQOPPPDLRSLGFGRRVRPPQERALLVVFTRSQRKNLFAEMREQLGSA 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                disorders, etc. (all claimed). AWFX proteins are also used for screening drugs or compounds that modulate AMFX protein activity or expression as well as to treat disorders characterized by insufficient or excessive production of AMFX protein.
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   Herrmann JL;
                                                                                                                                                                                                                                                                                                Claim 1; Page 44-45; 134pp; English.
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Matches 455; Conservative
Spytek KA, Rastelli L,
                                                          2001-626395/72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      455 AA;
                                                                                         N-PSDB; AAI70203
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vaccine; cancer; tumour; bone disorder; avascular necrosis; allergy; heamatopotetic disorder; immune disorder; endometriosis; renal disease; infection; inflammatory disease; lung disease; scleroderma; ataxia; bowel disease; appendicitis; blood disorder; cardiovascular disorder; graft versus host disease; GVHD; lymphaedema; brain disorder; occular disorder; hepatitis C virus infection; cardiac disorder; autosomal dominant deafness; PNNA-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel cytoplasmic, nuclear membrane bound and secreted NOVX polypeptides, useful for treating cancers and tumours, bone disorders, Paget's disease, haematopoietic disorders, spinal diseases and immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gangolii EA;
                                                                                                                                                      Human; growth/differentiation factor 6-like protein; NOVX; NOV9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Spaderna SK, Gangolii
Shimkets R, Mishra V;
Alsobrook JP, Liu X;
Peyman J, Stone D;
                                                                                                                              Human growth/differentiation factor 6-like protein NOV9.
421 VPTKLTPISILYIDAGNNVVYKQYEDMVVESCGCR
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Majumder K,
Grosse WM,
Smithson G,
                                                          AAU79173 standard; Protein; 455 AA
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20000S-226353P.
20000S-227085P.
20000S-227395P.
20000S-227600P.
20010S-27595P.
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2000US-225837P.
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                                                                                                         (first entry)
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Szekeres ES,
Ellerman K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Padigaru M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CURA-) CURAGEN CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Macdougall J;
                                                                                                         02-JUL-2002
                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                            16-AUG-2000;
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16-AUG-2000;
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22-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rastelli L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vernet CAM,
Gerlach VL,
                                                                                                                                                                                                                                                                                                             21-FEB-2002
                                                                                AAU79173;
                                            AAU79173
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The present invention relates to new isolated NOVX polypeptides named NOVI-NOV9. The invention can be used for identifying an agent (a cellular receptor or downstream effector) that binds to the polypeptide. The molecules of the invention are useful for treating or preventing wolvx-associated disorders in humans. The antibody of the invention is useful for determining the presence or amount of NoVX in a sample, and for treating a pathological state in a mammal. The method of the invention is useful for determining the presence of an amount of NOVX in a sample which is used as a marker for cancerous cell or tissue type. The molecules of the invention are useful in the manufacture of a medicament for treating or preventing cancer, tumour, bone disorders, any scular necrosis, allery, haematopoletic disorders, immune disorders, endometriosis, renal diseases, infections, inflammatory diseases, lung diseases, appendicitis, blood

Claim 1; Page 86; 234pp; English.

disorders

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421 VPTKLTPISILYIDAGNNVVYKQYEDMVVESCGCR 455
           06-JUN-2000;
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JL;
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disorders, cardiovascular disorders, graft versus host disease (GVHD), lymphaedema, brain disorders, ocular disorders, hepatitis C virus infection, cardiac disorders and autosomal dominant deafness (DFNA-2). The present amino acid sequence represents the human growth/differentiation factor 6-like protein NOV9 that is one of the NOVX proteins described in the invention.
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                                                                                                                                                                                                      SKSANTITSFVDRGLDDLSHTPLRRQKYLFDVSMLSDKEELVGAELRLFRQAPSAPWGPP
                                                                                                                                                                                                                EAAGPGAGAEGSWPPPSGAPDARPWLPSPGRRRRTAFASRHGKRHGKKSRLRCSKKPLH
                                                                                                                                                                                                                                                                                                                                 AGPLHVQLFPCLSPLLLDARTLDPQGAPPAGWEVFDVWQGLRHQPWKQLCLELRAAWGEL
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                                                                                       Length 455;
                                                                                                           Indels
                                                                                     Score 2447; DB 23;
Pred. No. 1.2e-199;
Mismatches 0;
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100.0%;
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                                                                                                           Conservative
                                                                                     Query Match
Best Local Similarity
                                                                   455 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200194587-A2
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                                                                                                         455;
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                                                                   Sequence
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The present invention relates to new extracellular messenger polypeptides and polynuclectides encoding them. XMES is useful in the diagnosis, treatment and prevention of neurological disorders (e.g. epilepsy, stroke, or Alzheimer's disease), autoimmune/inflammatory disorders (e.g. epilepsy, activated immune deficiency syndrome, AIDS, Addison's disease, or allergies), developmental disorders (e.g. renal tubular acidosis, anaemia or Cushing's syndrome), endocrine disorders (e.g. renal tubular acidosis, anaemia or cushing's syndrome), and cell proliferative disorders (e.g. annery, and in the assessment of the effects of exogenous compounds on the expression of nucleic acid and amino acid sequences of extracellular messengers. XMES may also be used in the treatment of viral, bacterial, fundal, parasitic, protozoal and helminthic infections, trauma, disorders associated with hypoptiuitarism, hypothyroidism, hyperthyroidism or gonadal steroid hormones, and hypothyroidism, hyperthyroidism or gonadal steroid hormones, and sequence is human XMES-6 protein.
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                                                                                                                                                                   Azimzai Y;
S, Hafalia A;
                                                                                                                                                                                                                                                                                                                                                                                        them, useful for diagnosing, treating or preventing e.g. neurological, autoimmune, inflammatory, developmental and endocrine disorders
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Duggan BM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 2437; DB 23;
Pred. No. 8.8e-199;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                            New extracellular messenger polypeptides and
                                                                                                                                                                 Walia
                                                                                                                                                                                             Baughn MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 113-114; 123pp; English.
                                                                                                                                                                   DB,
                                                                                                                                                                      Nguyen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 99.6%;
Best Local Similarity 99.8%;
Matches 454; Conservative
06-JUN-2000; 2000US-210233P.
23-JUN-2000; 2000US-213465P.
14-NOV-2000; 2000US-249019P.
                                                                                                                                                                                             Ľu Y,
                                                                                                             (INCY -) INCYTE GENOMICS INC
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Tang YT,
                                                                                                                                                                                                                                                                              WPI; 2002-154573/20.
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AAR95636;

AAR95636 RESULT

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GRGPRVVPHEYMLSIYRTYSIAEKLGINASFFQSSKSANTITSFVDRGLDDLSHTPLRRQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NVVYKQYEDMVVESCGCR 455
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Celeste AJ, Melton DA, Wozney JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HARD ) HARVARD COLLEGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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25-MAR-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequence represents cattle articular cartilage-derived morphogenetic protein-2 (CDMP-2). The N-terminal methionine and signal peptide is missing, but part of the pro-region, a typical proteolytic cleavage site and a C-terminal domain containing 7 highly conserved Cys residues characteristic of the transforming growth factor-beta gene family are present. A single N-glycosylation site is located in the pro-region. A consensus highly conserved motif in CDMP proteins (AAR95641) is present in the C-terminal domain. CDMP-2 is present in a purified cartilage extract (claimed) which stimulates local cartilage formation and repair when combined with a matrix and implanted in a mammal. The protein may be used in therapy of e.g. chondromalacia or osteoarthritis, to heal joint surfaces, or to repair cartilage after reconstructive surgery.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            proteins - used to stimulate the in vivo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               317.436
/note= "C-terminal mature domain"
/note= "Consensus conserved motif (AAR95641)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  / Match 73.5%; Score 1798; DB 17; Length 436; Local Similarity 80.8%; Pred. No. 1.8e-144; hes 354; Conservative 18; Mismatches 48; Indels 18.
                                                                                                                                                                                                                                                                        Cattle; cartilage-derived morphogenetic protein-2; CDMP-2; articular cartilage; chondrogenic; vulnerary; implantation; chondromalacia; osteoarthritis; therapy; joint repair.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       733.316
/note= "Proteolytic processing site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "N-glycosylation site"
421 VPTKLTPISILYIDAGNNVVYKQYEDMVVESGGCR 455
                                                                                                                                                                                                                                      Cartilage-derived morphogenetic protein-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New purified cartilage extracts and development and repair of cartilage
                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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                                                                                                                   AAR95636 standard; Protein; 436
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1996-251714/25.
N-PSDB; AAT31602.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modified-site
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                                                                                                                                                                                              25-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-MAY-1996
                                                                                                                                                                                                                                                                                                                                                         Bos taurus
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Peptide Domain

Region

Key

SSAELGSTKGMRSRKEGKMQRAPRDSDAGRE---GQEPQPRPQDEPR---AQQPRAQEPP 86

Sequence Query Match

Best Loca Matches 33

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317
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                                                                                                    377
                                                                                                                                               378 YEAYHCEGVCDFPLRSHLEPTNHAIIQTLMNSMDPGSTPPSCCVPTKLTPISILYIDAGN 437
                                                                            GAPDARPWLPSPGRRRRTAFASRHGKRHGKKSRLRCSKKPLHVNFKELGWDDWIIAPLE
                                                                                                             KYLFDVSMLSDKEELVGAELRLFRQAPSAPWGPPAGPLHVQLFPCLSPLLLDARTLDPQG
                                  207 APPAGWEVFDVWQGLRHQPWKQLCLELRAAW-GELDAGEAEARARGPQQPPPDLRSLGF
                                                                    GRRVRPPQERALLVVFTRSQRKNLFAEMREQLGSA-EAAGPGAGAEGSW-----PPPPS
                                                                                                                                                                                                                                                                                                  Bone morphogenetic protein; VL-1; tendon; ligament; tendinitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wolfman NM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rosen VA, Thomsen GH,
                                                                                                                                                                                                                                                                                  Human mature VL-1 (BMP-13) encoding sequence
                                                                                                                                                                                                                                                                                                                                         1.201
202.321
/label= mature protein
e 202.321
/note= "claimed"
- 220.321
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N-PSDB; AAQ96208.
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"Claim 5"

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/note=
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                                                                     07-DEC-1993;
                                                                                                             25-MAR-1994;
02-NOV-1994;
                                                                                                                                                                            Celeste AJ,
                                                                                          22-DEC-1994;
                               US5658882-A
                                                   19-AUG-1997
                                                                                                                                                                                     Wozney JM;
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                                                      BMP-12 related proteins are a subset of the BMP/TGF-beta/Vg-1

family of proteins, including BMP-12 and VL-1. VL-1 is designated
BMP-13. Like BMP-12, it is expected that BMP-13, as expressed by
mammalian cells such as CHO cells, exists as a hetrogeneous popn.

of active species of BMP-13 protein with varying N-termini. It is
ceppered that all active species will contain the AA sequence
beginning with the 19th Cys residue of the mature protein until
the 119th residue of the mature protein. Other active
after the 120th residue of the mature protein. Other active
species contain additional AA sequence in the N-terminal direction.
AAQ96208 is a partial DNA sequence and AAR78730 is the derived AA
sequence of a portion of the 2.5 kb DNA insert of the plasmid
subclone pGEMJLDC31/2.5, derived from clone lambdaJLDC31.
                                                                                                                                                                                                                                                                                                                      EXEAYHCEGVCDFPLRSHLEPTNHAIIQTLANSMDPGSTPPSCCVPTKLTPISILYIDAG 436
                                                                                                                                                                                                                                                                                                            LDARTLDPQGAPPAGWEVFDVWQGLRHQPWKQLCLELRAAWGELDAGEAEARARGPQQPP 256
                                                                                                                                                                                                                                                                                                                                                                                            SGAPDARPWLPSPGRRRRTAFASRHGKRHGKKSRLRCSKKPLHVNFKELGWDDWIIAPL 376
                                                                                                                                                                                                                                                                   137 DLSHTPLRRQKYLFDVSMLSDKEELVGAELRLFRQAPSAPWGPPAGPLHVQLFPCLSPLL 196
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                                                                                                                                                                                                                                                                                                                                                                                                      BMP-13; bone morphogenetic protein; human; tendon; ligament; wound healing; tissue repair; tendonitis; carpal tunnel syndrome;
          nseq
                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                                                          Length 321;
        morphogenetic proteins -12 and -13 and corresp. DNA -sn. for inducing tendon/ligament-like tissue formation
                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                          71.4%; Score 1747; DB 16;
100.0%; Pred. No. 2.7e-140;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human bone morphogenetic protein BMP-13.
                                     Claim 14; Page 62-64; 84pp; English.
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/label _ Sig_peptide
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/note= "Claim 5"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 319; Conservative
                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                                                       321 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-JAN-1998
                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                           Query Match
                    compsn.
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This polypeptide comprises a novel bone morphogenetic protein, designated BMP-13 that induces tendon and ligament formation. Its amno acid sequence was deduced from isolated genomic clone v1-1 (see AAT90386). A claimed method for inducing formation of tendon and/or ligament tissues involves the administration of a composition containing at least one protein selected from BMP-13, MP52 (see AAW26590) and BMP-12 (see AAW2689). The method is used for tissue (including skin) healing and repair. This is useful for treating tendonitis, carpal tunnel syndrome and other defects of traumatic or congenital origin, in cosmetic surgery and to improve fixation of tendons or ligaments to bone. The specified proteins can also be used to increase activity of other BMPs e.g. BMP-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       137 · DLSHTPLRRQKYLFDVSMLSDKEELVGAELRLFRQAPSAPWGPPAGPLHVQLFPCLSPLL 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LDARTLDPQGAPPAGWEVFDVWQGLRHQPWKQLCLELRAAWGELDAGEAEARARGPQQPP 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PPDLRSLGFGRRVRPPQERALLVVFTRSQRKNLFAEMREQLGSAEAAGPGAGAEGSWPPP 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SGAPDARPWLPSPGRRRRTAFASRHGKRHGKKSRLRCSKKPLHVNFKELGWDDWIIAPL 376
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Inducing tendon and ligament formation using BMP-12, BMP-13 or M - useful for tissue healing and repair, treatment of tendonitis, improving fixation of tendons to bone etc
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                                                                                                                                                                                                                                                                                                     Wolfman NM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71.4%; Score 1747; DB 18;
100.0%; Pred. No. 2.7e-140;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                     Melton DA, Rosen VA, Thomsen GH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 5; Column 57-60; 43pp; English.
                                                     94US-0362670.
93US-0164103.
94US-0217780.
94US-0333576.
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93US-0164103.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 100.
Matches 319; Conservative
                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1997-424270/39.
N-PSDB; AAT90386.
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DLSHTPLRRQKYLFDVSMLSDKEELVGAELRLFRQAPSAPWGPPAGPLHVQLFPCLSPLL 62

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RESULT 8
AAR78739
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a chimeric DNA comprising a DNA sequence encoding a propeptide from a member of the transforming growth factor (TGF)-beta superfamily of proteins. This DNA is linked to a DNA sequence encoding an amino acid sequence encoding a mature polypeptide consisting of Bone Morphogenetic Protein (BMP)-12, BMP-13 or MP52 protein. The DNA sequences are useful for producing proteins which induce tendon/ligament like tissue formation, and for isolating and cloning further DNA sequences encoding BMP-12 related proteins with similar activity. The proteins are useful for the induction of tendon/ligament-like tissue formation, wound healing, ligament and other tissue repair, augmenting the activity of bone morphogenetic proteins, and for treating tendonitis, the activity of bone morphogenetic proteins, and for treating tendonitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New chimeric DNAs, useful for treating tendonitis, carpal tunnel syndrome and other tendon and ligament defects, comprises DNA encoding propeptide linked to DNA encoding bone morphogenetic proteins (BMP)-12,
                                                                                                                                                 Human; bone morphogenic protein; BMP-13; vulnerary; antiinflammatory; analgesic; gene therapy; transforming growth factor-beta; TGF-beta; tissue formation; wound healing; tissue repair; ligament defect; VL-1; carpal tunnel syndrome; tendonitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tunnel syndrome and other tendon and ligament defects. The sequence is human VL-1 protein also designated as BMP-13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thomsen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71.4%; Score 1747; DB 22;
100.0%; Pred. No. 2.7e-140;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wolfman NM,
                                                                                                                                                                                                                                                                           1..201
/label= Signal_peptide
202..321
/label= Mature_BMP_12_protein
                                                                                                                        Human full length VL-1 or BMP-13 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; Column 57-60; 42pp; English.
                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rosen VA,
                            AAE10982 standard; Protein; 321 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                              94US-0362670.
93US-0164103.
94US-0217780.
94US-0333576.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GEMY ) GENETICS INST INC. (HARD ) HARVARD COLLEGE.
                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wozney JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-588978/66.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             321 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAD18333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BMP-13 or MP52
                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                      US6284872-B1
                                                                                                                                                                                                                                                                                                                                                                                                                   28-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                22-DEC-1994;
07-DEC-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-MAR-1994;
                                                                                         18-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                     04-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Celeste AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Melton DA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                           AAE10982;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               present
                                                                                                                                                                                                                                                                           Peptide
                                                                                                                                                                                                                                                                                                           Protein
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                                                                                                                                                                                                                                                                Key
              AAE10982
RESULT
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243 EYEAYHCEGVCDFPLRSHLEPTNHAIIQTLMNSMDPGSTPPSCCVPTKLTPISILYIDAG 302
                63 LDARTLDPOGAPPAGWEVFDVWOGLRHOPWKOLCLELRAAWGELDAGEARARGPQOPP 122
                                                             316
                                                                             376
                                                                                                                                                                                     EYEAYHCEGVCDFPLRSHLEPTNHAIIQTLMNSMDPGSTPPSCCVPTKLTPISILYIDAG 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oligos #6 and #7 (AAQ96218 & AAQ96219) are used as primers for the amplification of a 275 bp DNA probe, the internal 269 bp of which corresp. to nts #607 to #865 of AAQ96207, from the BMP-12 encoding plasmid subclone PCR1-1#2. This probe was radioactively labelled and used to screen a murine genomic library. DNA sequence analysis of one of positively hybridising recombinants named MNR32 indicates that it encodes a portion of the mouse gene corresp. to the PCR product mV2 (murine homolog of the human VL-1 sequence AAQ96213.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          - used in
197 LDARTLDPQGAPPAGWEVFDVWQGLRHQPWKQLCLELRAAWGELDAGEAEARARGPQQPP
                                                             257 PPDLRSLGFGRRVRPPQERALLVVFTRSQRKNLFAEMREQLGSAEAAGPGAGAEGSWPPP
                                                                                                                          SGAPDARPWLPSPGRRRRTAFASRHGKRHGKKSRLRCSKKPLHVNFKELGWDDWIIAPL
                                                                                                                                                       183 SGAPDARPWLPSPGRRRRTAFASRHGKRHGKKSRLRCSKKPLHVNFKELGWDDWIIAPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wolfman NM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          morphogenetic proteins -12 and -13 and corresp. DNA -sn. for inducing tendon/ligament-like tissue formation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bone morphogenetic protein; mV2; tendon; ligament.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rosen VA, Thomsen GH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                          AAR78739 standard; Protein; 263 AA.
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                                                                                                                                                                                                                                                  437 NNVVYKQYEDMVVESCGCR 455
                                                                                                                                                                                                                                                                 94WO-US14030
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94US-0217780
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                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HARD ) HARVARD COLLEGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1995-224320/29.
N-PSDB; AAQ96224.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-DEC-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-DEC-1993;
25-MAR-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Murine mV2
                                                                                                                                                                                                                                                                                                                                                                                        AAR78739;
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                                                                                                                                                                                                                                                                               303
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Gaps

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Indels

Conservative

Local Similarity es 319; Conserv

Matches 137

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DLSHTPLRRQKYLFDVSMLSDKEELVGAELRLFRQAPSAPWGPPAGPLHVQLFPCLSPLL 196

BMP-13 or MP-52 tendonitis,

4,

19;

DB 18; Length 263;

299

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419

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Mouse; bone morphogenic protein; BMP-12; vulnerary; antiinflammatory; analgesic; gene therapy; transforming growth factor-beta; TGF-beta; tissue formation; wound healing; tissue repair; ligament defect; carpal tunnel syndrome; tendonitis; mV2.
                                                                           This polypeptide comprises a fragment of a murine homologue of human bone morphogenetic protein 12 (BMP-13) (see also AMW2551). Its amino acid sequence was deduced from DNA subclone mV2 (see AAT903997), isolated from murine genomic DNA using primers (see AAT90393-94) based on human BMP-12 sequences. Human BMP-13, BMP-12 (see AAW25689) and MP52 (see AAW25690) polypeptides are used in a claimed method for inducing tendon and ligament formation.
                                                                                                                                                                                                                                                                          180 PAGPLHVQLFPCLSPLLLDARTLDPQGAPPAGWEVFDVWQGLRHQPWKQLCLELRAAWGE
                                                                                                                                                                                                                                                                                                                                                                   300 AEAAGPGAGAEGSWPPPSGAPDARPWLPSPGRRRRRTAFASRHGKRHGKKSRLRCSKKPL
                                                                                                                                                                                                                                                                                                                                                                                                                     360 HVNFKELGWDDWIIAPLEYEAYHCEGVCDFPLRSHLEPTNHAIIQTLMNSMDPGSTPPSC
                                                                                                                                                                                                                                                                                                                240 LDAGEAEARARGPQQPPPPDLRSLGFGRRVRPPQERALLVVFTRSQRKNLFAEMREQLGS
                                                                                                                                                                                                         Query Match 49.3%; Score 1207.5; DB 18; Lengt Best Local Similarity 83.7%; Pred. No. 1.6e-94; Matches 231; Conservative 6; Mismatches 20; Indels
 Inducing tendon and ligament formation using BMP-12, useful for tissue healing and repair, treatment of improving fixation of tendons to bone etc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        420 CVPTKLTPISILYIDAGNNVVYKQYEDMVVESCGCR 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       228 CVPTKLTPISILYIDAGNNVVYKQYEDMVVESCGCR 263
                                                    Example 1; Column 69-72; 43pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Encoded 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= Unknown
/note= "Encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAE10985 standard; Protein; 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= Unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Murine partial mV2 protein.
                                                                                                                                                                                  263 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-FEB-1997;
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                                                                                                                                                                                  Sequence
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AAE10985
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                                                                                                                                                                                 180 PAGPLHVQLFPCLSPLLLDARTLDPQGAPPAGWEVFDVWQGLRHQPWKQLCLELRAAWGE 239
                                                                                                                                                                  240 LDAGEAEARARGPQQPPPPDLRSLGFGRRVRPPQERALLVVFTRSQRKNLFAEMREQLGS 299
                                                                                                                                                                                                                    300 AEAAGPGAGAEGSWPPPSGAPDARPWLPSPGRRRRRTAFFASRHGKRHGKKSRLRCSKKPL 359
                                                                                                                                                                                                                                   112 AEA----AGAEGSCPAPSGSPDTGSWLPSPGRRRRRTAFASRHGKRGKKSRLRCSRKPL 167
                                                                                                                                                                                                                                                                      360 HVNFKELGWDDWIIAPLEYEAYHCEGVCDFPLRSHLEPTNHAIIQTLMNSMDPGSTPPSC 419
                                                                                                                                                                                                                                                                                  19; Gaps
                                                                                                                               BMP-13; bone morphogenetic protein; mouse; tendon; ligament; wound healing; tissue repair; carpal tunnel syndrome; tendonitis;
                                                                Length 263;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wolfman NM;
    AA
                                                              Score 1207.5; DB 16; Lengt
Pred. No. 1.6e-94;
6; Mismatches 20; Indels
 The partial DNA sequence of this subclone and corresp. translation are given in AAQ96224 & AAR78739.
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                                                                                                                                                                                                                                                                                                                        /label= Pro, Thr
/note= "encoded by RCC"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Murine BMP-13 homologue fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                  AAW26595 standard; Protein; 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94US-0362670.
93US-0164103.
94US-0217780.
94US-0333576.
                                                              Query Match
Best Local Similarity 83.7%;
Matches 231; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1997-424270/39.
                                     263 AA;
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Misc-difference
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07-DEC-1993;
25-MAR-1994;
02-NOV-1994;
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                                       Seguence
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4
                                                                                                                                                                                                                           The invention relates to a chimeric DNA comprising a DNA sequence encoding a propeptide from a member of the transforming growth factor (1GF)-beta superfamily of proteins. This DNA is linked to a DNA sequence encoding an amino acid sequence encoding a mature polypeptide consisting of Bone Morphogenetic Protein (BMP)-12, BMP-13 or MP52 protein. The DNA sequences are useful for producing proteins which induce tendon/ligament like tissue formation, and for isolating and cloning further DNA sequences encoding BMP-12 related proteins with similar activity. The proteins are useful for the induction of tendon/ligament-like tissue formation, wound healing, ligament and other tissue repair, augmenting the activity of bone morphogenetic proteins, and for treating tendonitis, carpal tunnel syndrome and other tendon and ligament defects. The present sequence is murine partial mV2 protein which is homologous to human BMP-12 or VL-1 sequences of the invention.
                                                                                                                                                New chimeric DNAs, useful for treating tendonitis, carpal tunnel syndrome and other tendon and ligament defects, comprises DNA encoding propeptide linked to DNA encoding bone morphogenetic proteins (BMP)-12,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      180 PAGPLHVQLFPCLSPLLLDARTLDPQGAPPAGWEVFDVWQGLRHQPWKQLCLELRAAWGE 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  240 LDAGEAEARARGPQQPPPDLRSLGFGRRVRPPQERALLVVFTRSQRKNLFAEMREQLGS 299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             360 HVNFKELGWDDWIIAPLEYEAYHCEGVCDFPLRSHLEPTNHAIIQTLMNSMDPGSTPPSC 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transforming growth factor-beta family; mitogenic; differentiation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 22; Length 263;
                                                                                                                                                                                                                                                                                                                                                                                                                                                19;
                                                                              Thomsen GH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New TGF-beta family member - MP-52 protein sequence.
                                                                              Wolfman NM,
                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1202.5; DB
Pred. No. 4.3e-94;
6; Mismatches 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; Column 71-74; 42pp; English.
                                                                              Rosen VA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR69600 standard; Protein; 501 AA
                                                                                                                                                                                                                                                                                                                                                                                                                           49.18;
93US-0164103.
94US-0217780.
94US-0333576.
                                            (GEMY ) GENETICS INST INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                              Wozney JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 230; Conservative
                                                         HARD ) HARVARD COLLEGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                              2001-588978/66.
                                                                                                                                                                                                                                                                                                                                                                                                     263 AA;
                                                                                                                            N-PSDB; AAD18336
                                                                                                                                                                                  BMP-13 or MP52
          25-MAR-1994;
02-NOV-1994;
 07-DEC-1993;
                                                                              Celeste AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-0CT-1995
                                                                                          Melton DA;
                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR69600;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52
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The amino acid sequence of a novel member of the transforming growth deactor-beta (TGF-b) family named Mp-52. The gene encodes a protein of 501 amino acids (AA). The protein, or at least the mature protein, has mitogenic and/or differentiation inducing properties useful in the treatment or prevention of diseases of bone, cartilage, connective tissue, skin, mucosa, epithelium or dental tissue. The protein can also be used for wound healing and tissue regeneration e.g. in osteoporosis
treatment; prevention; disease; bone; cartilage; connective tissue; skin; mucosa; epithelium; dental tissue; wound healing; osteoporosis; tissue regeneration; arthritis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ------PRAQEPPGRGPRVVPHEYMLSIYRTYSIAEKLGINASFFQ 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GQTGGLTQPKKDEPKKLP----PRPG-GPEPKPGHPPQTRQATARTVTPKGQLPGGKAP 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LCLELRAAWGELDAGEAEARARGPQQPPPPDLRSLGFGRRVRPPQERALLVVFTRSQRKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120 SSKSANTITSFVDRGLDDLSHTPLRRQKYLFDVSMLSDKEELVGAELRLFRQAPS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -APWGPPAGPLHVQLFPCLS----PLLLDARTLDPQGAPPAGWEVFDVWQGLRH-QPWKQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               L-FAEMREQLGSAEAAGPGAGAEGSWPPPSGAPDARPWLPSPGRRRRTAFASRHGKRHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 501;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              - and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New DNA encoding a new member of the TGF beta family related vectors, host cells etc., has mitogenic and differentiation inducing activity, e.g. for treating preventing diseases of bone and cartilage etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (BIOP-) BIOPHARM GES BIOTECHNOLOGISCHEN ENTWICKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38 GSTKGMRSRKEGKMQRAPRDSDAGREGQEPQPRPQDEPRAQQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Neidhardt H, Paulista M, Hoetten G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 927.5; DB 1
Pred. No. 2.3e-70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64; Mismatches
                                                                                                                                                                                                                        /label= mature protein
                                                                                                                                                                     Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                          93DE-4326829.
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94DE-4420157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1995-090897/12.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        501 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAQ83695
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                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                  09-AUG-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          10-AUG-1993;
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195 EAGLANTITSFIDKGQDDRGPV-VRKQRYVFDISAL-EKDGLLGAELRILRKKPSDTAKP 252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAT69695
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                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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          ------PRAQEPPGRGPRVVPHEYMLSIYRTYSIAEKLGINASFFQ 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | | | : | : :: | | | | | :| :| | GQTGGLTQPKKDEPKKLP----PRPG-GPEPKPGHPPQTRQATARTVTPKGQLPGGKAP 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PKAGSVPSSFLLKKAREPGPPREPKEPFRPPPITPHEYMLSLYRTLSDADRKGGNSSVKL 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SSKSANTITSFVDRGLDDLSHTPLRRQKYLFDVSMLSDKEELVGAELRLFRQAPS---- 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38 GSTKGMRSRKEGKMQRAPRDSDAGREGQEPQPRPQDEPRAQQ------7
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mature BMP can be produced by directly adding a BMP processing enzyme to a solution containing BMP precursor protein, or by transforming an animal cell with expression vectors containing DNA encoding the enzyme and precursor protein, culturing the transformant and isolating the mature BMP from the culture. The method can be used to produce MP52, BMP-2, BMP-4, BMP-6 and BMP-7, abhormalities.
                                                                                                                                                                                                                                                                                                                                                                                    by treatment of furin either
KKSRLRCSKKPLHVNFKELGWDDWIIAPLEYEAYHCEGVCDFPLRSHLEPTNHAIIQTLM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97;
                                                                                                                                                                                 BMP; processing enzyme; MP52;
bone formation; bone regeneration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is MP52, which is a bone morphogenetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
                                     NSMDPGSTPPSCCVPTKLTPISILYIDAGNNVVYKQYEDMVVESCGCR 455
                                               98; Indels
                                                                                                                                                                                                                                                                                                                                                                                   Production of mature bone morphogenetic protein. - by precursor protein with a processing enzyme such as fudirectly or by expressing them both in the same host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 927.5; DB 1
Pred. No. 2.3e-70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1; Pages 21-25; 34pp; Japanese
                                                                                                                                                                                                                                                                                                                                       Takahashi M;
                                                                                                                                                                                                                                                                                                           (FARH ) HOECHST YAKUHIN KOGYO KK.
                                                                                                       501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64;
                                                                                                                                                                                                                                                                                                                      (FARH ) HOECHST PHARM & CHEM KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37.9%;
                                                                                                                                                                                                                                                                                        96JP-0130618.
                                                                                                      AAW36100 standard; Protein;
                                                                                                                                                                                Bone morphogenetic protein;
BMP-2; BMP-4; BMP-6; BMP-7;
                                                                                                                                                                                                                                                                      97WO-JP01474
                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 209; Conservative
                                                                                                                                                                                                                                                                                                                                       Kimura M, Makishima F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1997-549748/50.
N-PSDB; AAT98191.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 501 AA;
                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                W09741250-A1
                                                                                                                                                                                                                                                                     28-APR-1997;
                                                                                                                                                                                                                                                                                        30-APR-1996;
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                                                                                                                                             08-MAY-1998
                                                                                                                                                                Human MP52
                                                                                                                         AAW36100;
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348
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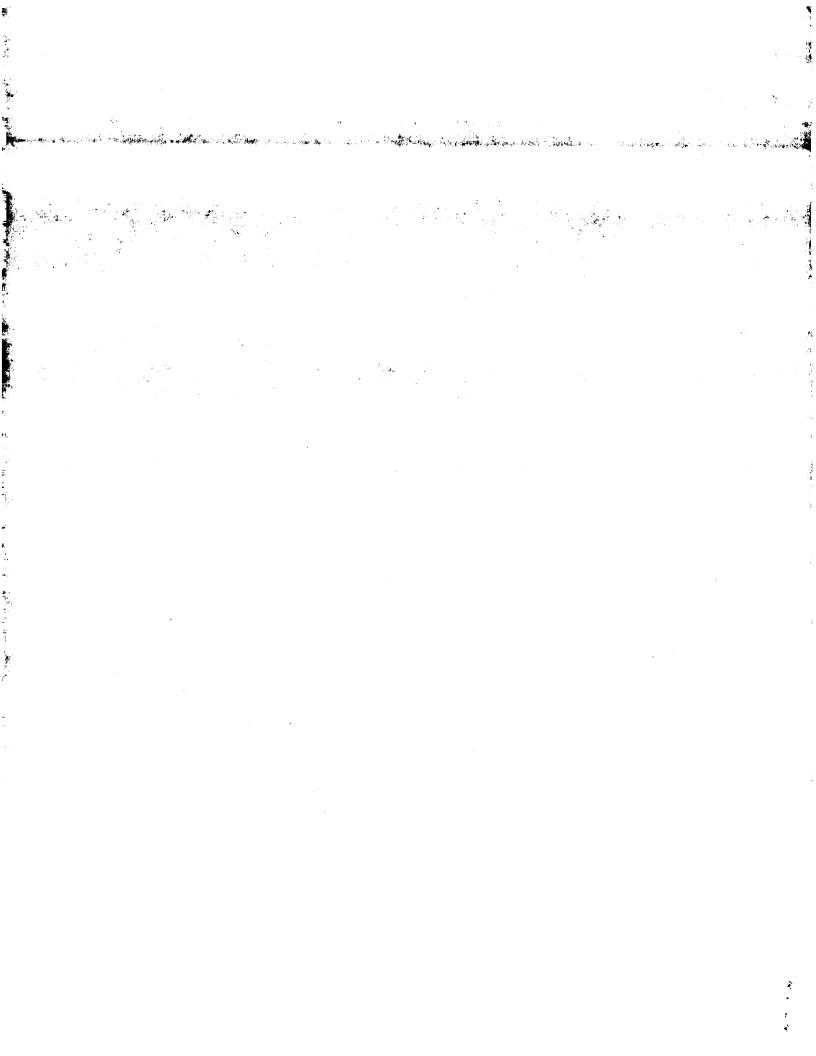
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This sequence is the human transforming growth factor (TGF)-beta protein designated MP52. MP52 can be used in a compound of formula (I): A-X(1-20)-B(1-20) (I); A = protein, or fragment, of the TGF-beta superfamily with cartilage and/or bone inducing activity (e.g. MP52); B = I or more substituent groups with an affinity to the extracellular matrix, caplular components of bone and/or cartilage and/or to a biocompatible carrier matrix; X = I or more covalent bonds and/or spacer groups. The compound may be used to inhibit bone resorption, prevent or treat bone or cartilage related disorders, including osteoporasis, Paget's disease, osteodystrophy, osteoarthris or osteoarthropathy and to treat bone or cartilage damage caused by wounding or overloading.
                                                                                                                                                                                                                                                                                                                                               407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human transforming growth factor-beta; TGF-beta; MP52; superfamily; cartilage; bone inducing activity; inhibit; bone resorption.
                                              253 AAPGGGRAAQL--KLSSCPSGRQPASLLDVRSV--PGLDGSGWEVFDIWKLFRNFKNSAQ
                                                                                                                                                                                            175 -APWGPPAGPLHVQLFPCLS----PLLLDARTLDPQGAPPAGWEVFDVWQGLRH-QPWKQ
                                                                                                                                                  LCLELRAAWGELDAGEAEARARGPQQPPPPDLRSLGFGRRVRPPQERALLVVFTRSQRKN
                                                                                                                                                                                                                                                                                                L-FAEMREQLGSAEAAGPGAGAEGSWPPPSGAPDARPWLPSPGRRRRTAFASRHGKRHG
                                                                                                                                                                                                                                                                                                                                                                                                                                               KKSRLRCSKKPLHVNFKELGWDDWIIAPLEYEAYHCEGVCDFPLRSHLEPTNHAIIQTLM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NSMDPGSTPPSCCVPTKLTPISILYIDAGNNVYYKQYEDMVVESCGCR 455
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95DE-1048476
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12-JUL-1995;
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                                                                            fractures
 Claim 1;
                                                                                             Sequence
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                                                                                                            Query Match
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                                                                                                                                  -APWGPPAGPLHVQLFPCLS----PLELDARTLDPQGAPPAGWEVFDVWQGLRH-QPWKQ 228
                                                                                                                                             347
                                                                                                                                                                                                                                              --PRAQEPPGRGPRVVPHEYMLSIYRTYSIAEKLGINASFFQ 119
                                                                            135 PKAGSVPSSFLLKKAREPGPPREPKEPFRPPPITPHEYMLSLYRTLSDADRKGGNSSVKL 194
                                                                                                            LCLELRAAWGELDAGEAEARARGPQQPPPDDLRSLGFGRRVRPPQERALLVVFTRSQRKN 288
                                                                                                                                                                                                                                      407
                                                                                                                                                                                                                                                                                                                                                                                               diferentiation; bone induction; osteoporosis; teeth; joint tissue; cartilage; mucous membrane; skin; nails; regeneration; skeletal disorder; fracture; dimer.
                                          353 LFFNEIKARSGODDKT-------VYEYLFSO-RRKRRAPLATROGKRPS 393
                  Gaps
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                                                                                                                                                                                                    L-FAEMREQLGSAEAAGPGAGAEGSWPPPSGAPDARPWLPSPGRRRRRTAFASRHGKRHG
                                                                                                                                                                                                                                                                                                                                                                                protein MP52, a growth/differentiation factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 High molecular weight human MP52 growth or differentiation factor promotes bone induction, is useful for treatment and prevention of bone disease
                                                                                                   SSKSANTITSFVDRGLDDLSHTPLRRQKYLFDVSMLSDKEELVGAELRLFRQAPS----
                                                                                                                                                                                                                                     KKSRLRCSKKPLHVNFKELGWDDWIIAPLEYEAYHCEGVCDFPLRSHLEPTNHAIIQTLM
                 97;
DB 18; Length 501;
                                                                                                                                                                                                                                                                      NSMDPGSTPPSCCVPTKLTPISILYIDAGNNVVXKQYEDMVVESCGCR 455
                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Takahashi
                98;
                                 38 GSTKGMRSRKEGKMQRAPRDSDAGREGQEPQPRPQDEPRAQQ--
37.9%; Score 927.5; DB 1
44.7%; Pred. No. 2.3e-70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Τ,
                64; Mismatches
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                                                                                                                                                                                                                                                                                                                              AAW11900 standard; Protein; 501
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(FARH ) HOECHST PHARM & CHEM KK.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96WO-JP02065.
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                                                                                                                                                                                                                                                                                                                                                                (first entry)
                Conservative
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        Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                factor;
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                209;
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Query Match
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Matches 2(
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                                                   AAWI1900 is a high mol. wt. form of a human growth/differentiation factor MP52. MP52 promotes bone induction and is useful for plastic reconstructive surgery, cosmetic facial treatment, bone transplantation and tooth implantation. It is also useful for the treatment and prevention of disorders of bone formation, bone, cartilage, joint tissue, skin, mucous membranes, nalls or teeth; for wound treatment and tissue regeneration; and for the treatment of skeletal disorders and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----PRAQEPPGRGPRVVPHEYMLSIYRTYSIAEKLGINASFFQ 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -APWGPPAGPLHVQLFPCLS----PLLLDARTLDPQGAPPAGWEVFDVWQGLRH-QPWKQ 228
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                                                                                                                                                                                                                                                                                                                                                             Length 501;
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44.7%; Pred. No. 2.3e-70;
iive 64; Mismatches 98
Page 12-16; 25pp; Japanese.
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                                                                                                                                                              The present sequence is the human MP52 protein, which is described in WO 9316099 and 9504819 as a member of the human transforming growth factor beta superfamily. Active MP52 can be used in a medicament to treat and prevent nervous system diseases, and/or to treat neuropathological conditions caused by nervous
                                                                                                   Medicaments contg. protein MP52 - useful for treating neurological
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44.7%; Pred. No. 2.3e-70;
iive 64; Mismatches 98; Indels 97;
                                    Paulista M, Pohl J, Unsicker K;
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                                                                                                                                       Claim 2; Pages 12-14; 21pp; German.
                                                                                                                                                                                                                                                                                 Query Match 37.99
Best Local Similarity 44.77
Matches 209; Conservative
                                    Hoetten G,
                                                            WPI; 1997-078343/08.
N-PSDB; AAT59405.
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                                    Bechtold R,
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Result No.

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L (Gases I to 343)

NH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

L Onpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

CDNA Library Preparation: Miklosel J. Brownstein (NHGRI), Shiraki

Toshiyuki and Placro Carninci (RIKEN)

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Right quality sequence stop: 532.

Location/Qualifiers
                                                         BO563481 9103,022,
AQ311900 RPCII1-94
BB637633 BB637633 BG162724 df17904.y
BIG162724 df17904.y
BIG162724 df17904.y
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AU241555 AU241555
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          AI761284 wh98b04.x
BI401488 MI-P-CP0-
BF688622 602185258
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BG186221 RST5070 A
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BG385196 306833 MA
A1478076 MPMGp621_
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 543)
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AL572764 AL572764
AL576612 AL576612
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                                                                                       BB637633
BB162724
BI473851
CNS01SYJ
AU241555
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BG969662
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CNS0442A
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BF045110
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BQ567172
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mRNA sequence.
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Homo sapiens
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VERSION
KEYWORDS
SOURCE
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TITLE
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COMMENT
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BI559439
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BE098696 UI-R-BJI-
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BF044119 BP250023A
BOL69372 STR00320
BF542757 UI-R-C3-s
                                                               November 25, 2002, 00:59:55; search time 2432 Seconds (without alignments) 9489.543 Million cell updates/sec
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Compugen Ltd.
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                                                                                                                                                                                 16154066 segs, 8097743376 residues
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         GenCore version
Copyright (c) 1993 - 2002
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Maximum Match 100%
Listing first 45 summaries
                                               nucleic search, using sw model
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Tel: 319 335 8260
Eax: 319 335 8265
Email: msoares@blue.weeg.ulowa.edu
Oligo-dr track not found, Not I site shown in beginning of sequence is likely internal to the message. cDNA Library Preparation: M.B. Soares in Clone distribution: clones will be available through
Bonaldo,M.F., Lennon,G. and Soares,M.B. Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCTCTCCGGAGACAGAAGTATTTGTTTGATGTGTCCATGCTCTCAGACAAAGAAGAGGTG 513
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                                                                                                                                         Program for Rat Gene Discovery and Mapping
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Pred. No. 9.2e-58;
); Mismatches 65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
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Seg primer: M13 Forward
POLYA-No.
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                                                                     Genome Res. 6 (9),
                                                                                                                                                                 University of Iowa
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                                                                                                /clome_host="bullog"
/lab_host="bullog"
/note="Organ: testis; Vector: pBluescriptR (modified
/note="Organ: testis; Vector: pBluescriptR (style="bullog: colorable"); Oligo-dr primed using primer s'-TTTTTTTTTTTTTTVN-3',
size-selected for average insert size 2.2 kb and
normalized to ROT 5. This is a primary library enriched
for full-length clones and constructed using the
Cap-trapper method (Carninci, in preparation). Library
constructed by M. Brownstein (NIMI/NHGRI, National
Institutes of Health). Note: this is a NIH_MGC Library."
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UI-R-BJ1-atb-h-03-0-UI.sl UI-R-BJ1 Rattus norvegicus cDNA clone
UI-R-BJ1-atb-h-03-0-UI 3', mRNA sequence.
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99.4%; Pred. No. 8.3e-95;
iive 0; Mismatches 3
                        /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5295441"
                                                                                           /clone_lib-"NIH_MGC_97"
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Rattus norvegicus
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Funding for cattle EST sequencing was provided by the USDA National Research Initiative, Animal Genome Resource Grant AG 99-3205-8534 to H. A. Lewin and J. E. Wonack. Base Calling/Quality Scores: PHRED from Washington University Genome Center. Vector Trimmi g: Cross_match from Washington University Genome Center PHRAP suite. This sequence is vector free and at least 200 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BF044119 563 bp mRNA linear EST 10-OCT-2000 BP250023A10F2 Soares normalized bovine placenta Bos taurus cDNA clone BP250023A10F2 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bovidae; Bovinae; Bos.
1 (bases 1 to 563)
Lewin,H.A., Soares,M.B., Rebeiz,M., Pardinas,J., Liu,L. and Larson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W. M. Keck Center for Comparative and Functional Genomics
University of Illinois at Urbana-Champaign
340 Edward R. Madigan Laboratory, 1201 W. Gregory Dr., Urbana, IL
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Insert Length: 563 Std Error: 0.00
Plate: BP250023A10 row: F column: 2
    u
                                                                     Score 303.4; I
Pred. No. 1.3e-
0; Mismatches
    68
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Fax: 217 244 5617
Email: h-lewin@uiuc.edu
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84.6%;
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Unpublished (2000)
                                                                                                                      Conservative
                                                                                             Similarity
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                                                                                                                      Matches 340;
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/clone="UI-R-C3-sq2" blo-UI"
/dev_stage="dault"
/dev_stage="dault"
/dev_stage="dault"
/dev_stage="dault"
/dev_stage="DH10B (Life Technologies)"
/note="Vector: pT773D-pac (Pharmacia) with a modified
polylihker; Site_1: Not I; Site_2: ECO RJ; The UI-R-C3
libraries from rat placenta, adult lung, brain, liver,
kidney, heart, spleen, ovary, muscle, and 8, 12 and 18-day
embryos, after a series of subtractions to reduce the
representation of cDNAs from which ESTs had already been
generated. The following serially subtracted libraries
were generated in this process: UI-R-C3, UI-R-C2,
/UI-R-A1, UI-R-B1. The tag is a string of 3-5
nucleotides present between the Not I site and the
oligo-dr track whichallows identification of the library
of origin of a clone within themixture. The subtracted
cDNA inserts from UI-R-C3 clones from which 3 ESTS had
been derived was used as a driver in a hybridization with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 University of Iowa 451 Encketain Medical Research Building Iowa City, IA 52242, USA 7e1: 319 335 8250
Fax: 319 335 9255
Email: msoares@blue.weeg.ulowa.edu
01190-dT track not found, Not I site shown in beginning of sequence 1s likely internal to the message. cDNA Library Preparation: M.B. Soares Lab Clone distribution: clones will be available through Research Genetics (www.resgen.com) This clone is also available through the I.M.A.G.E. Consortium at LLNL (info@image.llnl.gov).
Seq primer: M13 Forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the UT-R-C2P library in the form of single-stranded circles. The remaining single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DH10B bacteria (LifeTechnologies) to generate the UT-R-C3 library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 6:791-806, 1996).
                                                                                                                                                              EST 03-JUL-1999
                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae;
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Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                          AI535156 403 bp mRNA linear EST 03-JU UI-R-C3-sq-b-01-0-UI.S1 UI-R-C3 Rattus norvegicus cDNA clone UI-R-C3-sq-b-01-0-UI 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genome Res. 6 (9), 791-806 (1996) 97044477
814 AGTCTGGGCTTCGGCCGGAGGGTGCGGCC 842
                                                                                                                                                                                                                                                                                                                                              Chordata;
Rodentia;
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                        30 AGTCTGGGCTTCGGCCGGAGGGTGCGGCC
                                                                                                                                                                                                                                                     AI535156.1 GI:4449291
                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Soares, MB
                                                                                                                                                                                                                                                                                                                           Rattus norvegicus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          discovery
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AI535156/c
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MEDLINE
COMMENT
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AUTHORS
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KEYWORDS
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TITLE

SOURCE

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Email: thisse@igbmc.u-strasbg.fr

EST from a cDNA of a gene whose expression is spatially restricted during embryogenesis. We have established its expression pattern during embryonic development by whole mount in situ hybridization on zebrafish embryos from the gastrula stage to 2 days of development. The corresponding data are available on the zebrafish community database at http://zfin.org/cDNA library preparation: B. Riggleman. DNA Sequencing by:IGBMC sequencing facility. Clone distribution: zebrafish international resource center at the University of Oregon (Institute of Neuroscience, 1254 University of Oregon; Eugene, OR 97403-1254)

Seq primer: T3 ATTAACCCTCACTAAAGGGA.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /cloud_lb="segmentation stage cDNA library"
/dev_stage="segmentation stage embryos"
/note="vector: Lambda Zap; Site_1: EcoRI; Site_2: XhoI;
/ligo dT cDNA library constructed from RNA pooled from segmentation stage_zebrafish embryos"

169 c 172 g 119 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1005 GCTGCCCTCGCCCGGCCGCCGGCGCGCGCACGGCCTTCGCCAGTCGCCATGGCAAGCC 1064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1125 GCTGGGCTGGGACGACTGGATTATCGCGCCCCTGGAGTACGAGGCCTATCACTGCGAGGG 1184
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UI-R-C3-sq-b-01-0-UI.rl UI-R-C3 Rattus norvegicus cDNA clone
UI-R-C3-sq-b-01-0-UI 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1065 GCACGGCAAGAAGTCCAGGCTACGCTGCAGCAAGAAGCCCCTGCACGTGAACTTCAAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              318 ACTIGGAIGGGACGACIGGAICATCGCICCCTGGAITACGAAGCCTAICACTGCGAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCTGATGAACTCCATGGACCCCGGCTCCACCCCGCCCAGCTGCTGCGTGCCCACAATT
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Bonaldo,M.F., Lennon,G. and Soares,M.B.
                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Danio rerio"
/db_xref="taxon:7955"
/clone="CB278"
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BF542757
LOCUS
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B0169372.1 GI:20376800
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes
; Cyprinidae; Danio.
1 (bases 1 to 661)
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1, rue Laurent Files, BP163, CU de Strasbourg, 67404 IllKirch Cedex
                                                                                                                                                                                                                                      /sex="female"
/lab_host="DH10B"
/lab_host="DH10B"
/note="Organ: placenta: Vector: pT773Pac; Site_1: EcoRI;
/note="forgan: placenta: Vector: ptacenta: Vector: 
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-C. and Thisse, B.

-Cression of the zebrafish genome during embryogenesis (2002) Unpublished (2002)
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Contact: Thisse B
Institut de Genetique et de Biologie Moleculaire et Cellulaire
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                443 GCTGATGAACTCCATGACCCGGCTCCACCAGCCCGCCTGCTGCTCCAAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1;
                                                                                                                                                       /db_xref="taxon:9913"
/clone="BP250023A10F2"
/clone_lib="Soares normalized bovine placenta"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 12; Length 563;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 271.4; DB 1:
Pred. No. 2.4e-43;
0; Mismatches 11
      primer: AGCGGATAACAATTTCACACAGGA
                                  High quality sequence stop: 563.
Location/Qualifiers
                                                                                              1. .563
/organism="Bos taurus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19.0%;
96.0%;
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Fax: 33 3 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 289; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          France
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BQ169372
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EST 24-JUN-2002

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/strain="crossbreed"
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/db.ref="texon:9823"
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/lab.host="DH10B (Life Technologies)"
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/note="vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_I: Not I; Site_2: EcoRI; The MI-P-CP1
library is normalized library derived from the MI-P-CP0
library, ultimately derived from there MI-P-CP0
library, ultimately derived from which this clone
was derived, please visit our web site at
http://plgest.genome.iastate.edu/. The procedure used to
create this library has been previously described (Bonaldo
incon) and Soares, Genome Research 6: 791-806, 1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Iowa State University
201 Kildee Hall, Ames, IA 50011-3150, USA
1-15152944252
Eax: 5152944401
Email: cktuggle@iastate.edu
Tissue Procurement: Dr. Chris Tuggle, Iowa State University
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus. [1 (bases 1 to 798)]
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
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      679 GTGTGGCAGGGCCTGCGCCACCAGCCCTGGAAGCAGCTGTGGTTGGAGCTGCGGGCCGCA 738
                                      248 GTGTGGCAGGTCCTGCGCCCTCAGCCGTGGAACCAGCTGTGCTTGGAGCTTCGGGCAGTC 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genetics (www.resgen.com).

The following repetitive elements were found in this CDNA sequence: 1-86, >GC_rich#Low_complexity (matched compliment) Seq primer: MI3 FORWARD POLYA-No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Tuggle CK
Molecular Genetics Laboratory, Department of Animal Science
                                                                                                                                                                                                                                                                                                                                           BQ604531 798 bp mRNA linear EST 2
MI-P-CP1-nzc-d-04-0-UI.S1 MI-P-CP1 Sus scrofa cDNA clone
MI-P-CP1-nzc-d-04-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16.7%; Score 237.6; DB 14; Length 798; ilarity 74.3%; Pred. No. 1.1e-36; Conservative 0; Mismatches 104; Indels 0;
                                                                                                                                                             308 TGGGGTGAGCTGGACGCCAGGGATTCAGGAGCGCGC 343
                                                                                                                             739 TGGGCGAGCTGGACGCCGGGGAGGCCGAGGCGCGC 774
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227 c
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Sus scrofa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organisms="Katchus norvegicus"
/strain="Sprague-Dabley"
/db_xref="taxon:10116"
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/dlone_lib="ul-R-G3"
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/lab_nost="bull to the technologies"
/dab_nost="bull to the technologies"
/dap_nost="bull to the technologies"
/dab_nost="bull to the technologies"
/dap_nost="bull t
                                                                                                                                                                                                                                                                                                    Email: msoares@blue.weeg.ulowa.edu
cDNA Library Preparation: M.B. Soares Lab Clone distribution:
clones will be available through Research Genetics (www.resgen.com)
This clone is also available through the I.M.A.G.E. Consortium at
LLNL (info@image.llnl.gov). IMAGE ID= 1768988
Seq primer: M13 Forward.
Location/Qualifiers
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Normalization and subtraction: two approaches to facilitate gene
                                                                                                                   Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Ecstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         439 GAICTCTCGCACACTCCTCTCCGGAGACAGAATTTGTTTGATGTCTCCATGCTCTCA 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           559 TGGGGCCACCACCAGGCGCTCCACGTGCACGTCTTCCTTTCCTTTTCGCCCCTACTG 618
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0; Mismatches 54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Rattus norvegicus"
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                                discovery
Genome Res. 6 (9), 791-806 (1996)
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Contact: Tuggle CK
Molecular Genetics Laboratory, Department of Animal Science
Towa State University
201 Kildee Hall, Ames, IA 50011-3150, USA
Tel: 5152944252
Fax: 5152944261
Email: Cktuggledisatate.edu
Oligo-dT track not found, Not I site shown in beginning of sequence
is likely internal to the message. CDNA Library Preparation: M.B.
Soares Lab, University of Iowa Clone distribution: clones will be available
through Research Genetics (www.resgen.com) The following repetitive
elements were found in this CDNA sequence: 1-86,
SGC_IICH#LOW_COMPLEXITY
Seg primer: M13 Forward
POLYA=NO.
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MI-P-CP0-nvn-c-04-0-UI.S1 MI-P-CP0 Sus scrofa cDNA clone
MI-P-CP0-nvn-c-04-0-UI 3', mRNA sequence.
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Sus.
                                                                                                                                                                                                                                                                                                                                                                                    1116 CTTCAAGGAGCTGGGCTGGACTGGATTATCGCGCCCTGGAGTACGAGGCCTATCA 1175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1235
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                                                                                                                                                                                                                                                                                          1056 TGGCAAGCGGCACGGCAAGAAGTCCAGGCTACGCTGCAGCAAGAAGCCCCTGCACGTGAA 1115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .296 CACCAAATTGACTCCCATCAGCATTCTATACATCGACGCGGGCAATAATGTGGTCTACAA 1355
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                                                                                                                                                                                                                                                                                                                                       68 GGGCCGGGGCCACGGGGCCAGGGGCCGGAGCCGCTGCAGCCGCAAGCCGTTGCACGTGGA 127
                                                                                                                                                                                                                                                                                                                                                                                                                                   128 CTTCAAGGAGCTCGGCTGGGACGACTGGATCATCGCGCCGCTGGACTACGAGGCGTACCA 187
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
1 (bases 1 to 505)
                                                                                                Length 475;
                                                                                                                                               0; Mismatches 105; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1356 GCAGTACGAGGACATGGTGGTGGAGTCGTGCGGCTGCAGGTAGCG 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 237; DB 9;
Pred. No. 1.3e-36;
  Soares and M.Fatima Bonaldo."
159 c 172 g 62 t
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1..505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BI401488.1 GI:15180549
                                                                                              16.68;
74.18;
                                                                                                                                                  Matches 300; Conservative
                                                                                                                            Similarity
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                             82 a
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                                                                                                                              Best Local
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                             SASE COUNT
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BI401488
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SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Emmail: cgapbs-rémail.nih.gov
Tissue Procurement: Ash Alizadeh, John Byrd, M.D., Mike Grever,
Tissue Procurement: Ash Alizadeh, John Byrd, M.D., Mike Grever,
M.D., Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLML at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 2190 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 453.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AI761284 475 bp mRNA linear EST 20-DEC-1999 wh98b04.xl NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2388751 3' similar to SW:GDF7_MOUSE P43029 GROWTH/DIFFERENTIATION FACTOR 7 PRECURSOR; contains TAR1.t3 TAR1 repetitive element; mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 475)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                       1116 CTTCAAGGAGCTGGGCTGGGACGACTGGTTATCGCGCCCCTGGAGTACGAGGCCTATCA 1175
                                                                                                                                                                                                                                                                                     1236 CATCCAGACGCTGATGAACTCCATGGACCCCGGCTCCACCCCGCCCAGCTGCTGCTGCTGCT 1295
                                                                                                                                                                                                                                                                                                                                                                                 1296 CACCAAATTGACTCCCATCAGCATTCTATACATCGACGGGGCAATAATGTGGTCTACAA 1355
1056 TGGCAAGCGGCACGGCAAGAAGTCCAGGCTACGCTGCAGCAAGAAGCCCCTGCACGTGAA 1115
                                                                                                                       128 CTTCAAGGAGCTGGGCTGGGATGACTGGATCATTGCGCCGCTGGACTACGAGGCGTACCA 187
                                                                                                                                                                                                                                                                                                              248 CATTCAGACGCTACTGAACTCTATGGCGCCGCGGCGCGCCGCCCCCTGCTGCGTGCCC 307
                                                                                                                                                                                                                                                                                                                                                                                                          68 GGCCGGGCCCACGGCCGCAGAAGCCGGAGCCGCTGTAGCCGCAAGCCACTGCACGTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
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/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1356 GCAGTACGAGGACATGGTGGTGGAGTCGTGCGGCTGCAGGTAGC 1399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        368 GCAATACGAGGACATGGTAGTGGAGGCGTGCGGCTGCAGGTAGC 411
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AI761284.1 GI:5176951
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AUTHORS
TITLE
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AI761284
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/clone_linable.nrH_MGC_43"
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/tissue_type="normal pigmented retinal epithelium"
/tissue_type="normal pigmented retinal epithelium"
/tissue_type="normal pigmented retinal epithelium"
/tissue_type="normal"
/tissue_typ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopteryqii; Neopteryqii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
1 (bases 1 to 552)
Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M., Eddy,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Mylie,T., Underwood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1021 CGCCGGCGGCGCGCACGGCCTTCGCCAGTCGCCATGGCAAGCGGCACGGCAAGAAGTCC 1080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1141 TGGATTATCGCGCCCCTGGAGTACGAGGCCTATCACTGCGAGGGTGTATGCGACTTCCCG 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1201 CTGCGCTCGCACCTGGAGCCCACCAACCACGCCATCATCCAGACGCTGATGAACTCCATG 1260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1261 GACCCCGGCTCCACCCCGCCCAGCTGCTGCGTGCCCAAATTGACTCCCATCAGCATT 1320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1321 CTATACATCGACGCGGCAATAATGTGGTCTACAAGCAGTACGAGGACATGG---TGGTG 1377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Albalish Washu MPIMG EST Danio rerio cDNA clone IMAGE:3721260 5' similar to TR:012938 012938 DYNAMO PROTEIN PRECURSOR.; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1081 AGGCTACGCTGCAGCAAGAAGCCCCTGCACGTGAACTTCAAGGAGCTGGGCTGGGACGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1025;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 230.8; DB 12; Length
Pred. No. 2.3e-35;
0; Mismatches 97; Indels
  found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAGTCGTGCGCTGCAGGTAGCGGTGCCTTTCCCGCCGCCTT 1419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           http://image.llnl.gov
Plate: LicMil57 row: c column: 16
High quality sequence stop: 715.
Location/Qualifiers
1..1025
                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                              /clone="IMAGE:4299591"
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75.1%;
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A1641304.1
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Best Local S
Matches 302
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DEFINITION
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AI641304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1025)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTTCAAGGAGCTGGGCTGGGACGACTGGATTATCGCGCCCCTGGAGTACGAGGCCTATCA 1175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                996 CAGGCCTTGGCTGCCTCGCCCGGCCGCCGCGGCGCGCCCACGCCCTTCGCCAGTCGCCA 1055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1056 TGGCAAGCGCCACGGCAAGAAGTCCAGGCTACGCTGCAGCAAGAAGCCCCTGCACGTGAA 1115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1296 CACCAAATTGACTCCCATCAGCATTCTATACATCGACGCGGGCAATAATGTGGTCTACAA 1355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            127
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 CAGGCGCCGCCGCACTGGCCGGACGCGCGCGCCCAGGGCAGCGGCGCGGGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1236 CATCCAGACGCTGATGAACTCCATGGACCCCGGCTCCACCCCGCCCAGCTGCTGCGTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           248 CATTCAGACGCTACTGAACTCTATGCGCCCGGATGCGGCCCCAGCCTCCTGCTGCGCGCC
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 236; DB 13; Length 505;
Pred. No. 2.1e-36;
0; Mismatches 105; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCAGTACGAGGACATGGTGGTGGAGTCGTGCGGCTGCAGGTAGC 1399
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="MI-P-CP0-nvn-c-04-0-UI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
/organism="Sus scrofa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BF688622
BF688622.1 GI:11974030
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 16.6%;
Best Local Similarity 74.0%;
Matches 299; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mRNA sequence.
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/lab_host="1">
/Lisu_Lype="1"/
/lab_host="XL1-blue MRF"
/lab_host="XL1-blue MRF"
/note="Vector: pSPORTI; Site_1: NotI; Site_2: SalI; Ist
strand CDNA was primed with a Not I - oligo(dT)15 primer
(5 peacTAGTTCTAGATCGGGGGGGCGCCCTTTTTTTTTTTTTT];
double-stranded cDNA was ligated to Sal I adaptors (BRL),
digested with Not I and cloned into the Not I and Sal I
sites of the pSPORTI vector (BRL). Library was constructed
by Matthew Clark (Lehrach lab; ICRF, London and Max Planck
Institut fuer Molekulare Genetik, Berlin). CDNAs for EST
analysis were selected following oligonucleotide
hybridization fingerprinting of arrayed clones from
zebzafish late somitogenesis (25 ss), adult liver or
embryonic shield stage (3.6 h) libraries. Fingerprint
data were used to computationally cluster cDNAs, and a
single CDNA from each cluster was chosen for sequencing.
In some cases multiple members of the same cluster were
sequenced to assess clustering parameters or single clones
were sequenced additional times to assess quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                 Email: 2brafish@watson.wustl.edu

CDNA Library Preparation: Matthew Clark. CDNA Library Arrayed by:

Matthew Clark. DNA Sequencing by: Washington University Genome
Sequencing Center Clone distribution: Genome Systems, St. Louis,

Missouri (web address: www.genomesystems.com) (email contact:

Info@eqonomesystems.com) and Research Genetics, Huntsville, Alabama
(web address: www.resgen.com) (email contact: info@resgen.com) and
RessourcenZentrumPrimarDatenbank, Berlin, Germany (web address:
Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R., and Wilson,R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="26 somite embryos, adult livers, shield
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                    4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Danio rerio"
/db_xref="taxon.7955"
/clone="IMAGE:3721260"
/clone_lib="Zebrafish WashU MPIMG EST"
/sex="mixed"
                                                                                                                                                          Unpublished (1998)
Contact: Stephen L. Johnson
Washington University School of Medicine
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                                                                                                                           WashU Zebrafish EST Project 1998
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High quality sequence stop: 475.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                Tel: 314 286 1800
Fax: 314 286 1810
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Email: msoares@blue.weeg.ulowa.edu
Oligo-dr track not found, Not I site shown in beginning of sequence
is likely internal to the message. CDNA Library Preparation: M.B.
Soares Lab Clone distribution: clones will be available through
                                                                                                                                                                                                                                                                               BF420157 307 bp mRNA linear EST 28-NOV-2000 UI-R-BJ2-bpj-f-01-0-UI.sl UI-R-BJ2 Rattus norvegicus cDNA clone UI-R-BJ2-bpj-f-01-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bonaldo,M.F., Lennon,G. and Soares,M.B. Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            451 Eckstein Medical Research Building Iowa City, IA 52242, USA Tel: 319 335 8250
Fax: 319 335 9565
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1266 CGGCTCCACCCCCCCCAGCTGCTGCGTGCCCACCAAATTGACTCCCATCAGCATTCTATA
                   305 CATTGACGCAGGAAATAATGTTGTGTACAAGCAGTATGAAGACATGGTAGTGGAGTCCTG
                                                                        1326 CATCGACGCGGCCAATAATGTGGTCTACAAGCAGTACGAGGACATGGTGGTGGTGGAGTCGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36;
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Seg primer: M13 Forward
POLYA-No.
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Rattus norvegicus
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/clone="qi03h02"
/clone="qi03h02"
/clone="qi03h02"
/sex="male and female"
/sex="male and female"
/dev_stage="Post natal day 5 to 13"
/dev_stage="Post natal day 5 to 13"
/note="organ: Organ of Corti; Vector: pBluescript; The Organ of Corti (Or) was fine dissected from a total of 386 or as follows: 102 samples from post-natal (P) day 5; 72 from Post from Post 102 from Post 102 samples from Post-natal (P) day 5; 72 from Post 102 and 24 from Post 103 from Post 103 from Post 104 from Post
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gi03h02.y1 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA clone gi03h02.y. mRNA sequence.
BQ563481.1 GI:21466450
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contains of gene expression in the mouse Organ of Corti at the onset of hearing of the mouse Organ of Corti at the onset of hearing of Doublished (2002)

Contact: Kachar, B.

Structural Cell Biology
National Institute of Deafness and other Communication Disorders 50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA
Tel: 301-402-1599
Fax: 301-402-1765
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chordata, Craniata, Vertebrata, Euteleostomi,
Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                       1125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1126 CTGGGCTGGGACGACTGGATTATCGCGCCCTGGAGTACGAGGCCTATCACTGCGAGGGT 1185
                                                                                                                                                                                                            1006 CTGCCCTCGCCCGGCCGCCGCGGCGCGCCACGCCTTCGCCAGTCGCCATGGCAAGCGG 1065
                                                                                                        109 CTGCCCTCGCCCGGCCGCGCGCGCGCACCGCCCTCAGCAGCCGTCACGCGAAGCGA 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                228
                                                                     GGCGCGGGCCCGAGGGGTCGTGGCCGCCGCCGTCGGGCGCCCCCGGATGCCAGGCCTTGG
                                                                                                                                                                                                                                                                                                                                                               1066 CACGGCAAGAAGTCCAGGCTACGCTGCAGCAAGAAGCCCCTGCACGTGAACTTCAAGGAG
                                                                                                                                                                                                                                                                                                                                                                                                          169 CACGGCAAGAAGTCCAGGCTGCGCTGCAGCAAAACCTCTGCACGTGAATTTTAAGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         229 TTAGGCTGGGACGATGGATTATCGCGCCCCTAGAGTACGAGGCCTATACACTGCGAGGGC
1 CGCAAGAACCTGTTCACTGAGATGCATGAGCAGCTGGGGCTCTGCAGAGGCTGCCGGA---
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Plate: 03 row: h column: 02
Seq primer: M13RP1 reverse primer (ABI).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
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Mammalia; Eutheria;
1 (bases 1 to 479)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     479
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TITLE
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COMMENT
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KEYWORDS
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LOCUS

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from Stratagene (La Jolla, AL, (Carally, E.S.), according to manufacturer's instructions. Briefly, 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker- primer and transcribed using Molloney murine leukemia virus reverse transcriptase (MMLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase. Ingated with EcoR I adapters in the presence of ligase and digested with Xho I. The CDNA was sequentially size fractionated over Pharmacias ize Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for CDNA greater than 400bp and 1000 bp. respectively. The CDNA was then directionally ligated to the Uni-ZAP XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with Gigapak II Gold and, upon titration on XLI Blue MRF' cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's ExAssist Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual CDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purificed from the phage clusted culture with the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          strength Biggs terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POP5 polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have I copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have know function; 45% of have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTS and 20% are unidentified."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Concert96(TM) plasmid purification kit (Invitrogen, carisbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the CDNA clones were generated with the universal M13 reverse primer (CAGGAAACAGCTATGACC) and 25%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
Gigapack III Gold Cloning kit (catalog # 237612), both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1021 CGCCGGCGCGCGCCCCCCCCCCAGCCCATGGCAAGCGGCACGGCAAGAAGTCC 1080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1081 AGGCTACGCTGCAGCAAGAAGCCCCTGCACGTGAACTTCAAGGAGCTGGGCTGGGACGAC 1140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1141 TGGATTATCGCGCCCCTGGAGTACGAGGCCTATCACTGCGAGGGTGTATGCGACTTCCCG 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1201 CTGCGCTCGCACCTGGAGCCCACCAACCACGCCATCATCCAGACGCTGATGAACTCCATG 1260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             324 CGGCGGAAACGCCGGGCCCCATTGGCCAATCGCCAGGGCAAGCGACCAGCAAGAACCTC 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25
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BE114678.1
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                                                           Norway rat.
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Matches 219;
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                   VERSION
KEYWORDS
SOURCE
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                                                                                                                                                                       AUTHORS
   ACCESSION
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                                                                                                                                                                                       TITLE
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                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E. (Abases 1 to 283)

Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P. and Venter, J. C. Upublished (1998)

V. Drer, Grass: RPCIII-94N16.TJ

Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Fat: 301 838 0200
Fax: 301 838 0200
                                      283 bp DNA linear GSS 04-MAY-1999
Homo sapiens genomic clone RPCI-11-94N16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://Dacpac.med.buffalo.edu/ordering) or from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BEI14678
UI-R-BJ1-awo-a-02-0-UI.sl UI-R-BJ1 Rattus norvegicus cDNA clone UI-R-BJ1-awo-a-02-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCIll Human Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      299 CGCGCGTGGTGCCCCACGAGTACATGCTGTCAATCTACAGGACTTACTCCATCGCTGAGA 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             163 AGCTGGGCATCAATGCCAGCTTTTTCCAGTCTTCCAAGTCGACTAGATACGATCACAGCT 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       359 AGCTGGGCATCAATGCCAGCTTTTTCCAGTCTTCCAAGTCGGCTAATACGATCACCAGCT
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 191.6; DB 17; Length
Pred. No. 9.7e-28;
0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="CDB:753639"
/db_xref="taxon:9606"
/clone="RRCI-11-94N16"
/clone_lib="RPCI-11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         83 g
                                                      RPCI11-94N16.TV RPCI-11
                                                                                                              AQ311900.1 GI:4043649
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Best Local Similarity 98.0%;
Matches 194; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              419 TTGTAGACAGGGGACTAG 436
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                                                                         DNA sequence.
                                                                                                                                                                       Homo sapiens
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                                                                                                              VERSION
KEYWORDS
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                                                                                                                                                                                                                                             AUTHORS
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/Strain="Stardue-Bulley"
/Strain="Stardue-Bulley"
/db_xref="taxon:10116"
/clone_lib="UT-R-Bil-awo-a-02-0-UI"
/clone_lib="UT-R-Bil-awo-a-02-0-UI"
/clone_lib="WetOr: pT739-Pac (Pharmacia) with a modified
/note="vector: pT739-Pac (Pharmacia) with a modified
polylinker; Site_l: Not I; Site_2: Eco RI; The UI-R-Bil
library is a subtracted library derived from the following
tissues: atrium at 16.5 dpc, ventricle at 16.5 dpc, AV
canal at 16.5 dpc, atrium at 15 dpc, ventricle at 15 dpc, AV
canal at 16.5 dpc, ventricle at 13 dpc, and adult heart.
For a detailed description of the library from which this
clone was derived, please visit our web site at
ratest.eng.ulowa.edu. The subtraction has been previously
described in (Bonaldo, Lennon and Soares, Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: msoares@blue.weeg.uiowa.edu
Oligo-dr track not found, Not I site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.B.
Soares Lab Clone distribution: clones will be available through
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                           Bonaldo,M.F., Lennon,G. and Soares,M.B. Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        572 CCGGGCCGCTCCACGTGCAGCTCTTCCCTTGCCTTTCGCCCTACTGCTGGACGCGCGGA 631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                632 CCCTGGACCCGCAGGGGGCGCCGCCGGCCGGCTGGGAAGTCTTCGACGTGTGGCAGGGCC 691
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                                                                                                                                                          Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242,
TTE: 319 335 8260
Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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80.8%; Pred. No. 4.1e-27;
iive 0; Mismatches 52

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    /organism="Rattus norvegicus"

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Seg primer: M13 Forward
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GI:8506783
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Murine mV2 protein

Perfect score:

Sequence:

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TGF beta-like clon
Murine protein MF5
Human MF-52 DNA.
Cartilage-derived
Human TGF-beta MF5
GDF-7 C-terminal r
CDNA encoding huma
Human bone inducin
Murine mV1 protein
Murine BMP-12 homo
                GDF-6 gene. Mus s
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Human osteoblast d
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CDNA encoding huma
DNA encoding human
Human bone morphog
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human growth/differentiation factor-6-like protein AMF10 DNA
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ABQ88241
AAQ83695
AAT69695
AAT69412
AAT59405
AAT59405
AAT88340
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AAT46150
AAT70296
AAQ96223
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AAD18335
AAQ96207
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AAQ96209
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AAD18316
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AAT31601
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31..96
/*tag= b
97..1395
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DNA encoding human
Human extracellula
Human bone morphog
Human full length
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Murine partial mV2
                                                                                                                                              November 24, 2002, 23:26:25; Search time 310 Seconds (without alignments) 10351.928 Million cell updates/sec
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Cartilage-derived
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Compugen Ltd.
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                  GenCore version
Copyright (c) 1993 - 2002
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Maximum Match 100%
Listing first 45 summaries
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Score

Result Š.

Nucleotide sequenc Mutant human MP52 DNA encoding novel

Murine bone morpho Murine clone, mV2 Fusion of BMP-2 pr

Human bone morphog Human bone morphog Human bone morphog Growth differentia

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The present sequence is that of DNA clone ACO1136_A. This includes an open reading frame that encodes the novel, secreted human growth/differentiation factor-6 (GDF6)-like protein, AMF10 (see AAM50216). AMF10 is expressed in astrocytoma and glioma-derived tissue. DNA encoding the AMF8 may be useful in gene therapy, and the protein may also be used as a therapeutic, especially in treatment of cancer and other cell proliferative disorders. Generally, the AMF1-10 (AMFX) nucleic acids and proteins of the invention are useful for treating or preventing AMFX-associated disorders, e.g. a disorder cell adhesion or migration pathway modulation, chemoresistance, radiotherapy resistance, survival in trophic factor limited secondary tissue site microenvironments, connective tissue disorders, tissue remodeling, oncogenesis, cancer of the breast, ovary, cervix, prostate, endometrium, stomach, colon, lung, bladder, kidney, brain, and soft-tissue, cellular transformation, developmental tissue remodeling, inflammation, blood clot formation and resorption, haematopoiesis, andiopensess, multidrug resistance related to organic anion transporters, malignant disease progression, autocrine and paracrine regulation of cell growth, and cellular responses to external stimuli, and other disease cellular responses to external stimuli, and other cellular responses.
                                                                                                                                                                                                                                     New AMF1-10 polypeptides and encoding polynucleotides, useful for treating or preventing disorders related to modulation of cell movement, cell signal processing, cell adhesion or migration pathways
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                                                                             Fernandes E
Herrmann JL;
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                                                                             Burgess CE,
Rastelli L,
                           (CURA-) CURAGEN CORP
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P-PSDB; AAM50216.
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1140 1020 1080 1080 1200 1200 1260 480 900 099 999 720 720 780 780 900 006 960 GGACCCCAGCAACCGCCCCCCCGACCTGCGGAGTCTGGGCTTCGGCCGCGAGGGTGCGG 1141 TGGATTATCGCGCCCCTGGAGTACGAGGCCTATCACTGCGAGGGTGTATGCGACTTCCCG CAGGCGCCCTCAGCGCCCTGGGGGCCACCAGCCGGGCCGCTCCACGTGCAGCTCTTCCCT TGCCTTTGGCCCCTACTGCTGGACGCGCGGACCCTGGACCCGCAGGGGGCGCCGCCGCCGCCGCC CCTCCCCAGGAGGGGGCCCTGCTGGTGTATTCACCAGATCCCAGCGCAAGAACCTGTTC GGGTCGTGGCCGCCGCCGTCGGGCGCCCCGGATGCCAGGCCTTGGCTGCCCTCGCCCGGC CGCCGGCGGCGCGCACGGCCTTCGCCAGTCGCCATGGCAAGCGGCACGCAAGAAGTCC CGCCGGCGCGCGCACGCCTTCGCCAGTCGCCATGGCAAGCGGCACGGCAAGAAGTCC AGGCTACGCTGCAGCAAGAAGCCCCTGCACGTGAACTTCAAGGAGCTGGGCTGGGACGAC 1141 TGGATTATCGCGCCCCTGGAGTACGAGGCCTATCACTGCGAGGGTGTATGCGACTTCCCG GACCCCGGCTCCACCCCGCCCAGCTGCTGCCGTGCCCACCAAATTGACTCCCATCAGCATT CTATACATCGACGCGGGCAATAATGTGGGTCTACAAGCAGTACGAGGACATGGTGGTGGTGGA GTAGACAGGGGACTAGACGATCTCGCACACTCCTCCCGGAGACAGAAGTATTTGTTT GTAGACAGGGGACTAGACGATCTCTCGCACACTCCTCTCCGGAGACAGAAGTATTTGTTT GGCTGGGAAGTCTTCGACGTGTGGCAGGGCCTGCGCCACCAGCCGTGGAAGCAGCTGTGC CCTCCCCAGGAGCGGCCCTGCTGGTGGTATTCACCAGATCCCAGGCGCAAGAACCTGTTC GCAGAGATGCGCGAGCAGCTGGGCTCGGCCGAGGCTGCGGGCCCGGGCGCGCGGGGGCGCCGAG TCGTGCGGCTGCAGGTAGCGGTGCCTTTCCCGCCGCCCTTGGCCCG 1425 1081 1081 421 481 601 721 781 841 1021 1021 1201 1201 1261 1261 1321 1321 1381 421 541 541 601 661 661 721 781 841 901 901 961 961 1381 481 δ g δ g οy g Qγ d ŏ g QY a δ q à 셤 ò g δ g οy g Qγ QΩ ò qq ò Op Óλ g δ Dp ò qq

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to new isolated NOVX polypeptides named NOVI-NOV9. The invention can be used for identifying an agent (a cellular receptor or downstream effector) that binds to the polypeptide. The molecules of the invention are useful for treating or preventing NOVX-associated disorders in humans. The antibody of the invention is useful for determining the presence or amount of NOVX in a sample, and for treating a pathological state in a mammal. The method of the invention is useful for determining the presence of an amount of NOVX in a sample which is used as a marker for cancerous cell or tissue type. The molecules of the invention are useful in the manufacture of a medicament for treating or preventing cancer, tumour, bone disorders, avascular necrosis, allergy, haematopoietic disorders, immune disorders,
                                                                                                                                                                                           vaccine; cancer; tumour; bone disorder; avascular necrosis; allergy; haematopoietic disorder; immune disorder; endometriosis; renal disease; infection; inflammatory disease; lung disease; scleroderma; ataxia; bowel disease; appendicitis; blood disorder; cardiovascular disorder; graft versus host disease; GVHD: lymphaedema; brain disorder; ocular disorder; hepatitis C virus infection; cardiac disorder; autosomal dominant deafness; DFNA-2; ds.
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/*tag= a
/product= "Human growth/differentiation factor 6-like
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                                                                                                                                      human growth/differentiation factor 6-like protein NOV9.
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                                                                                                                                                                          Human; growth/differentiation factor 6-like protein; NOVX; NOV9;
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Shimkets R, Mishra V,
Alsobrook JP, Liu X;
Peyman J, Stone D;
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Majumder K,
Grosse WM,
Smithson G,
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2000us-226236P
2000us-226353P
2000us-227085P
2000us-227492P
2000us-227492P
                    ABK48393 standard; DNA; 1425
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14-MAR-2001; 2001US-275952P
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Vernet CAM, Szekeres ES,
Gerlach VL, Ellerman K,
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23-AUG-2000;
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diseases, scleroderma, ataxia, bowel diseases, appendicitis, blood disorders, cardiovascular disorders, graft versus host disease (GVHD), lymphaedema, brain disorders, ocular disorders, hepatitis C virus infection, cardiac disorders and autosomal dominant deafness (DFNA-2). The present nucleic acid sequence encodes the human growth/differentiation factor 6-like protein NOV9 that is one of the
    infections, inflammatory diseases, lung
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                                                                                                                                                                                  Sequence 1425 BP; 234 A; 488 C; 469 G; 234 T; 0 other;
                                                                                                                                                                                                                        Query Match 100.0%; Score 1425; DB 24, Best Local Similarity 100.0%; Pred. No. 6.7e-246. Matches 1425; Conservative 0; Mismatches 0;
                                                                                                                                         NOVX proteins described in the invention.
endometriosis, renal diseases,
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841 CCTCCCCAGGAGCGGGCCCTGCTGGTGTTTCACCAGATCCCAGCGCAAGAACCTGTTC
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The present invention relates to new extracellular messenger polypeptides and polynucleotides encoding them. XMES is useful in the diagnosis, treatment and prevention of neurological disorders (e.g. epilepsy, stroke, or Alzhehmer's disease), autoimmune/inflammatory disorders (e.g. rallergies), developmental disorders (e.g. renal tubular acidosis, anaemia or Cushing's syndrome), endocraine disorders (e.g. renal tubular acidosis, anaemia or Cushing's syndrome), and cell proliferative disorders (e.g. cancer), and in the assessment of the effects of exogenous compounds on the expression of nucleic acid and amino acid sequences of extracellular messengers. XMES may also be used in the treatment of viral, bacterial, fungal, parasitic, protozoal and helminthic infections, trauma, disorders associated with hypoptuitarism, hypothyroidism or gonadal steroid hormones, and proper such as type I or type II diabetes mellitus. The XMES may be used for somatic or germline gene therapy. The present sequence is human XMES<sup>2</sup> CDNA.
                                                                                                                   Azimzai Y;
S, Hafalia A;
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                                                                                                                   juyen DB, Walia N, Gandhi AR,
Y, Baughn MR, Duggan BM, Lee
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Pred. No. 2.5e-245;
); Mismatches 2;
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                                                                                                                     Nguyen DB,
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23-JUN-2000;
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BMP-13; bone morphogenetic protein; human; tendon; ligament; wound healing; tissue repair; tendonitis; carpal tunnel syndrome;

Location/Qualifiers 2..967

Key

Homo sapiens

therapy; ss.

/*tag= a 2.604 /*tag= b 605.964 /*tag= c

sig_peptide

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bone morphogenetic protein BMP-13 gene clone vl-1.

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Inducing tendon and ligament formation using BMP-12, BMP-13 or MP-52 - useful for tissue healing and repair, treatment of tendonitis, improving fixation of tendons to bone etc

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Wolfman

GH,

Thomsen

Rosen VA,

Celeste AJ, Melton DA,

Wozney JM;

WPI; 1997-424270/39. P-PSDB; AAW26591.

94US-0362670. 93US-0164103. 94US-0217780.

> 07-DEC-1993; 25-MAR-1994; 02-NOV-1994;

22-DEC-1994;

94US-0333576

(GEMY) GENETICS INST INC. (HARD) HARVARD COLLEGE.

93US-0164103

07-DEC-1993;

US5658882-A

19-AUG-1997

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                                             This nucleotide sequence, designated v1-1, encodes a novel bone morphogenetic protein (see AAW26591), designated BMP-13. It was isolated from a human genomic library using a probe (see AAF90398) based on a partial BMP-13 sequence. A claimed method for inducing formation of tendon and/or ligament tissues involves administration of a composition containing at least one protein selected from BMP-13, MP52 (see AAW36590) and BMP-12 (see AAW36589). The method is used for tissue (including skin) healing and repair. This is useful for treating tendonitis, carpal tunnel syndrome and other defects of traumatic or congenital origin, in cosmetic surgery and to improve fixation of tendons or ligaments to bone. The specified proteins can also be used to increase activity of other BMPs e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 GATCTCGCACACTCCTCTCGGAGACACAGAGTATTGTTTGATGTGTCTCCATGCTCTCA
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Pred. No. 1.2e-167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69.3%; Scor.
100.0%; Pred. No. 1...
0; Mismatches
Example 1; Column 55-58; 43pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 69.3
Best Local Similarity 100.
Matches 987; Conservative
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DNA; 1171 BP

standard;

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RESULT 4
AAT90386
ID AAT9

(first entry)

21-JAN-1998

XX AC

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; bone morphogenic protein; BMP-13; vulnerary; antiinflammatory; analgasic; gene therapy; transforming growth factor-beta; TGF-beta; tissue formation; wound healing; tissue repair; ligament defect; VL-1; carpal tunnel syndrome; tendonitis; ds.
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              GTGTGGCAGGCCTGCGCCACCAGCCCTGGAAGCAGCTGTGTGCTTGGAGCTGCGGGCCGCA
                                                                  CTGCTGGTGGTATTCACCAGATCCCAGCGCAAGAACCTGTTCGCAGAGATGCGCGAGCAG
                                                                                                                                    CTGCTGGTGGTATTCACCAGATCCCAGCGCAAGAACCTGTTCGCAGAGATGCGCGGGCAG
                                                                                                                                                 CTGGGCTCGGCCGAGGCTGCGGGCCCGGGCGCGCGCGCCCGAGGGGTCGTGGCCGCCGCCGCCG
                                                                                                                                                                                                                                                                                                                                                                  CGGTGCCTTTCCCGCCGCCTTGGCCCG 1425
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human full length VL-1 or BMP-13 DNA.
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The invention relates to a chimeric DNA comprising a DNA sequence encoding a propeptide from a member of the transforming growth factor (TGF)-berts superfamily of proteins. This DNA is linked to a DNA sequence encoding an amino acid sequence encoding a mature polypeptide consisting of Bone Morphogenetic Protein (BMP)-12, BMP-13 or MP52 protein. The DNA sequences are useful for producing proteins which induce tendon/ligament like tissue formation, and for isolating and cloning further DNA sequences encoding BMP-12 related proteins with similar activity. The proteins are useful for the induction of tendon/ligament-like tissue formation, wound healing, ligament and other tissue repair, augmenting the activity of bone morphogenetic proteins, and for treating tendonitis, carpal tunnel syndrome and other tendon and ligament defects. The present sequence is human VL-1 DNA fragment also designated as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New chimeric DNAs, useful for treating tendonitis, carpal tunnel syndrome and other tendon and ligament defects, comprises DNA encoding propeptide linked to DNA encoding bone morphogenetic proteins (BMP)-12. BMP-13 or MP52 -
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                                                                              /product= "Human VL-1 protein"
/note= "CDS does not include start codon"
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100.0%; Pred. No. 1.2e-167;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                              "Mature VL-1 protein'
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Location/Qualifiers
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93US-0164103.
94US-0217780.
94US-0333576.
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07-DEC-1993;
25-MAR-1994;
02-NOV-1994;
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                                                                                                                                                                      sig_peptide
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                                                                                                                                                                                                                             mat_peptide
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                                                                              CTGCTGGTGGTATTCACCAGATCCCAGCGCAAGAACCTGTTCGCAGAGATGCGCGAGCAG
                                                                                                  CTGGGCTCGGCCGAGGCTGCGGGCCCGGGCGGGGGCCGAGGGGGTCGTGGCCGCCGCCG
                                                                                                                                            AAGCCCCTGCACGTGAACTTCAAGGAGCTGGGCTGGGACGACTGGATTATCGCGCCCCTG
                                                                                                                                                                                       GAGTACGAGGCCTATCACTGCGAGGGTGTATGCGACTTCCCGCTGCGCTCGCACCTGGAG
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          Human mature VL-1 (BMP-13) encoding sequence.
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EMP-12 related proteins are a subset of the BMP/TGF-beta/Vg-1 family of proteins, including BMP-12 and VL-1. VL-1 is designated bmp-13. Like BMP-12, it is expected that BMP-13, as expressed by mammalian cells such as CHO cells, exists as a hetrogeneous popn. Of active species of BMP-13 protein with varying N-termini. It is expected that all active species will contain the As sequence beginning with the 19th Cys residue of the mature protein until the stop codon after the 120th residue of the mature protein. Other active species contain additional As sequence in the N-terminal direction. AAQ96208 is a partial DNA sequence and AAR78730 is the derived AA sequence of a pottion of the 2.5 kb DNA insert of the plasmid subclone pGBMJLDC31/2.5, derived from clone lambdaJLDC31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              439 GAICTCTCGCACACTCCTCCGGAGACAGAGTATTTGTTTGATGTGTCCATGCTCTCA 498
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/note= "degenerate codes used due to poor print
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10; Mismatches
Location/Qualifiers
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94US-0217780
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Matches 969; Conservative
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25-MAR-1994;
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The sequence encodes cattle articular cartilage-derived morphogenetic protein-2 (CDMP-2). Primers AAT13603-06, constructed from conserved motific from bone morphogenetic protein, have been used in reverse transcription-polymerase chain reaction amplification of a cattle articular chondrocyte cDNA library, generating products of 120 and 280 bp, which are then used to screen a cattle articular cartilage CDNA library. The 5'-end with the N-terminal methionine codon and signal peptide sequence is missing. CDMP-2 is present in a purified cartilage extract (claimed) which stimulates local cartilage formation and repair when combined with a matrix and implanted in a mammal. The protein may be used in therapy of e.g. chondromalacia or osteoarthritis, to heal joint surfaces, or to repair cartilage after
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                                               Mature CDMP-2 C-terminal domain
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                   /*tag= a
/product= Mature CDMP-2 C-terminal d
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/note= "RT-PCR-amplified probe used
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P-PSDB; AAR95636.
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                                                        CGCCGCCCGGCCGGGAAGTCTTCGACGTGTGGCAGGGCCTGCGCCACCAGCCCTGGA
                                                                                   AGCAGCTGTGCTTGGAGCTGCGGGCCGCATGG---GGCGAGCTGGACGCCGGGGAGGCCG
                                                                                                               AGGCGCGCGCGCGGGGACCCCAGCAACCGCCGCCCCCGGACCTGCGGAGTCTGGGCTTCG
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                    GGCTCTTTCGCCAGGCGCCCTCAGCGCCCTGGGGGCCACCAGCCGGGCCGCTCCACGTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           119 CAGCTGTGCGTGCAGTTGCGGGCAGCCTGGGGTGAGCTGGACCCCGGGGATACGGGGGCG
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BMP-13; bone morphogenetic protein; mouse; tendon; ligament; wound healing; tissue repair; carpal tunnel syndrome; tendonitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BMP-13 or M
tendonitis,
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Pred. No. 2.9e-95;
1; Mismatches 84; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1046 BP; 212 A; 314 C; 331 G; 187 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Inducing tendon and ligament formation using BMP-12, - useful for tissue healing and repair, treatment of improving fixation of tendons to bone etc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thomsen GH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; Column 69-72; 43pp; English.
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                                                                                                                                               Location/Qualifiers
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93US-0164103.
94US-0217780.
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Best Local Similarity 87.2%;
Matches 675; Conservative
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25-MAR-1994;
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                                                                                                                                                                                                                                                                                                                                  Mouse; bone morphogenic protein; BMP-12; vulnerary; antiinflammatory; analgesic; gene therapy; transforming growth factor-beta; TGF-beta; tissue formation; wound healing; tissue repair; ligament defect; carpal tunnel syndrome; tendonitis; mV2; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                          not
GGAGCCGAGGGGTCATGTCCAGCGCCGTCGGGCTCCCCAGACACCGGGTCTTGGCTGCCC
                                                AAGAAGTCCAGGCTACGCTGCAGCAAGAAGCCCCTGCACGTGAACTTCAAGGAGCTGGGC
                                                      GACTTCCCGCTGCGCTCGCACCTGGAGCCCACCACCACGCCATCATCCAGACGCTGATG
                                                                                                                      ATCAGCATTCTATACATCGACGCGGCAATAATGTGGTCTACAAGCAGTACGAGGACATG
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                       TGGGACGACTGGATTATCGCGCCCCTGGAGTACGAGGCCTATCACTGCGAGGGTGTATGC
                                                                                               TGGGACGACTGGATTATCGCGCCCCTAGAGTACGAGGCCTATCACTGCGAGGGCGTGTGC
                                                                                                                                             AACTCCATGGACCCCGGCTCCACCCCGCCCAGCTGCTGCGTGCCCACCAAATTGACTCCC
                                                                                                                                                                                                            GTGGTGGAGTCGTGCGGCTGCAGGTAGCGGTGCCTTTCCCGGCCGCCTTGGCCCG 1425
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                                                                                                                                                                                                                   Thomsen GH;
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                                                                                                                                                                                                                                                                                                                                                                                                       /product= "Murine partial mV2 protein"
/transl_except= (pos:160..163, aa:Xaa)
/transl_except= (pos:740..742, aa:Xaa)
/note= "Xaa is an unknown amino acid; C
include start codon"
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94US-0217780.
94US-0333576.
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) HARVARD COLLEGE.
                                                                                                                                                                                                                                                                                                                  Murine partial mV2 DNA.
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25-MAR-1994;
02-NOV-1994;
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The invention relates to a chimeric DNA comprising a DNA sequence encoding a propetide from a member of the transforming growth factor (TGF)-beta superfamily of proteins. This DNA is linked to a DNA sequence encoding an amino acid sequence encoding a mature polypeptide consisting of Bone Morphogenetic Protein (BMP)-12, BMP-13 or MP52 protein. The DNA sequences are useful for producing proteins which induce tendon/ligament like tissue formation, and for isolating and cloning further DNA sequences encoding BMP-12 related proteins with similar activity. The proteins are useful for the induction of tendon/ligament-like tissue formation, wound healing, ligament and other tissue repair, augmenting the activity of bone morphogenetic proteins, and for treating tendonitis, carpal tunnel syndrome and other tendon and ligament defects. The present sequence is murine partial mV2 DNA which is homologous to human BMP-12 or VL-1 sequences of the invention.
                                                                                                                          new cnimeric DNAs, useful for treating tendonitis, carpal tunnel syndrome and other tendon and ligament defects, comprises DNA encoding propeptide linked to DNA encoding bone morphogenetic proteins (BMP)-12, BMP-13 or MP52 -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 581.8; DB 2
Pred. No. 2.9e-95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
                                                                                                                                                                                                                                                                                                 Example 1; Column 71-74; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 40.8%;
Best Local Similarity 87.2%;
Matches 675; Conservative
                                                     2001-588978/66
                                                                                    P-PSDB; AAE10985
DA;
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                                                                                       1371
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         - used in
AACTCCATGGACCCCGGCTCCACCCCGCCCAGCTGCGTGCCCACCAAATTGACTCCC
                         ATCAGCATTCTATACATCGACGCGGCAATAATGTGGTCTACAAGCAGTACGAGGACATG
                                                                                                              GTGGTGGAGTCGTGCGGCTGCAGGTAGCGGTGCCTTTCCCGCCGCCTTGGCCCG 1425
                                                                                                                                                                                                 Wolfman NM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       for inducing tendon/ligament-like tissue formation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    morphogenetic proteins -12 and -13 and corresp. DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1046 BP; 212 A; 314 C; 331 G; 187 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bone morphogenetic protein; mV2; tendon; ligament; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thomsen GH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
2..790
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/label= A,C,T or
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                                                                                                                                                                                                                                                                                                                                   DNA; 1046
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93US-0164103.
94US-0217780.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94WO-US14030
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Melton DA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             *tag=
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                                                                                                                                                                                                                                                                                                                                   AAQ96224 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Murine mV2 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   misc_difference
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07-DEC-1993;
25-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-DEC-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                   23-NOV-1995
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Wozney JM;
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                                                                                                                                                                                                                                                                                                                                                                              AAQ96224;
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1191
 1311
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 1131
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 526
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 298
 951
 711
 Gaps
 653 CGCCGGCCGGCTGGGAAGTC-TTCGACGTGTGGCAGGGCCTGCGCCACCAGCCCTGGAAG
 712 CAGCTGTGCTTGGAGCTGCGGGCCGCATGGGGCGAGCTGGACGCCGGGGAGGCCGAGGCG
 952 GGCGCCGAGGGGTCGTGGCCGCCGCCGTCGGGCCCCCGGGATGCCAGGCCTTGGCTGCCT
 1252 AACTCCATGGACCCGGCTCCACCCGCCCAGCTGCTGCGTGCCCACCAAATTGACTCCC
 647 AACTCCATGGACCCGGGCTCCACCCGGCCTAGCTGCTGCGTTCCCACAAACTGACTCCC
 1312 ATCAGCATTCTATACATCGACGCGGGCAATAATGTGGTCTACAAGCAGTACGAGGACATG
 CGCGCGCGGGGACCCCAGCAACCGCCCCCCGGACCTGCGGAGTCTGGGCTTCGGCCGG
 AGGGTGCGGCCTCCCCAGGAGCGGGCCCTGCTGGTGGTATTCACCAGATCCCAGCGCAAG
 892 AACCTGTTCGCAGAGATGCGCGGGGCAGCTGGGCTCGGCCGAGGCTGCGGGCCCGGGCGCG
 1012 TCGCCCGGCCGCCGCCGCCGCCGCCATCGCCAGTCGCCATGGCAAGCGGCACGGC
 1072 AAGAAGTCCAGGCTACGCTGCAGCAAGAAGCCCCTGCACGTGAACTTCAAGGAGCTGGGC
 1132 TGGGACGACTGGATTATCGCGCCCCTGGAGTACGAGGCCTATCACTGCGAGGGTGTATGC
 1372 GIGGIGGAGICGIGCGGCIGCAGGIAGCGIGCCITICCCGCCGCCCTIGGCCCG 1425
 14;
 Growth differentiation factor-6; GDF-6; transforming growth factor-beta; TGF-beta; cell proliferation;
 Indels
Score 581.2; DB lb;
Pred. No. 3.7e-95;
 0; Mismatches
 BP,
 40.8%;
87.2%;
 530
 (first entry)
 Conservative
 DNA;
 AAQ84280 standard;
 Best Local Similarity
Matches 675; Conserv
 pancreas; ss
 17-AUG-1995
 GDF-6 gene
 AAQ84280;
 Mus sp
 832
 1192
 167
 772
 RESULT 11
AAQ84280
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(first entry)
 477; Conservative
 WPI; 2000-531418/48.
P-PSDB; AAB12986.
 Similarity
 Huynh T;
 1398
 530
 29-NOV-2000
 15-JUN-1998;
 15-APR-1996;
 US6090563-A
 18-JUL-2000
 1396 TAG
 Query Match
 Local
 Mus sp.
 Lee S,
 Matches
 109
 61
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 RESULT 12
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 GGCAATAATGTGGTCTACAAGCAGTACGAGGACATGGTGGTGGAGTCGTGCGGCTGCAGG 1395
 108
 167
 Primer SJL141 (given in AAQ84278), based on a region spanning 2 Trp residues conserved in TGF-beta proteins, and primer SJL145 (AAQ84279) spanning the invariant Cys residues near the C-terminus were used to amplify mouse genomic DNA. New growth differentiation factor-6
 287
 347
 856 GCCCTGCTGGTGGTATTCACCAGATCCCAGCGCAAGAACCTGTTCGCAGAGATGCGCGAG 915
 916 CAGCTGGGCTCGGCCGAGGCTGCGGGCCCGGGGGGCGCCCGAGGGGTCGTGGCCGCCG 975
 407
 527
 Gaps
 1036 ACGCCCTTCGCCAGTCGCCATGCCAAGCGCCACGCCAAGAAGTCCAGGCTACGCTGCAGC
 228 AGAAAGCCTCTGCACGTGAATTTTAAGGAGTTAGGCTGGGACGACTGGATTATCGCGCCC
 1156 CTGGAGTACGAGGCCTATCACTGCGAGGCTGTATGCGACTTCCCGCTGCGCTCGCACCTG
 CCGCCCAGCTGCGTGCCCACCAATTGACTCCCATCAGCATTCTATACATCGACGCG
 168 ACCGCCTTCGCCAGCCGTCACGGCAAGCGACATGGCAAGAAGTCCAGGCTGCGCTGCAGC
 1216 GAGCCCACCAACCACGCCATCATCCAGACGCTGATGAACTCCATGGACCCCGGCTCCACC
 13;
 DB 16; Length 530;
 family, useful to treat cell proliferation disorders in pancreatic tissue
 to amplify mouse genomic DNA. New growth differentiation (AAQ84280) was identified from a mixture of PCR products.
 Indels
 Sequence 530 BP; 104 A; 166 C; 160 G; 100 T; 0 other;
 53;
 Query Match 28.9%; Score 412.2; DB 1
Best Local Similarity 87.8%; Pred. No. 5.8e-65;
Matches 477; Conservative 0; Mismatches 53
 Disclosure; Page 31-32; 62pp; English.
 (UYJO) UNIV JOHNS HOPKINS SCHOOL MED
 Location/Qualifiers
126..530
/*tag= a
 94WO-US07762
 93US-0089300
 WPI; 1995-066738/09.
 Lee S;
 P-PSDB; AAR66867
 08-JUL-1994;
 09-JUL-1993;
 WO9501801-A
 19-JAN-1995
 Huynh T,
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This invention relates to an antibody that specifically binds to a growth differentiation factor-6 (GDF-6) polypeptide. GDF-6 is a member of the transforming growth factor-beta (TGF-beta) family of proteins, and is expressed in placental tissue. The antibody of the invention can be used to identify tissue samples of placental origin. It may also be used to treat choriocarcinomas, or detect primary and metastatic neoplasms of placental origin. The antibodies may also be used to treat call proliferative diseases, and GDD-6 may be used as an indicator of developmental anomalies in prenatal screening procedures. The present sequence represents DNA encoding the murine GDF-6 protein.
 1035
 1036 ACGGCCTTCGCCAGTCGCCATGGCAAGCGGCACGGCAAGAAGTCCAGGCTACGCTGCAGC 1095
 167
 Antibody; growth differentiation factor-6; GDF-6; placenta; mouse; transforming growth factor-beta; TGF-beta; choriocarcinoma; neoplasm; detection; treatment; cell proliferative disease; ds.
 975
 856 GCCCTGCTGGTGGTATTCACCAGATCCCAGCGCAAGAACCTGTTCGCAGAGATGCGCGAG 915
 Gaps
 9
 CCGTCGGGCCCCCGGGATGCCAGGCCTTGGCTGCCCTCGCCCGGCGGCGGCGGCGGCGCGC
 916 CAGCTGGGCTCGCCCGAGGCTGCGGGCCCGGGCGCGGCGCCGAGGGGTCGTGGCCGCCG
 Antibody for detecting cell proliferative disorder associated w growth differentiation factor-6 expression, specifically binds growth differentiation factor-6 polypeptide
 13;
 28.9%; Score 412.2; DB 21; Length 530; 87.8%; Pred. No. 5.8e-65;
 Murine growth differentiation factor-6 (GDF-6) DNA sequence.
 Indels
 Sequence 530 BP; 104 A; 166 C; 160 G; 100 T; 0 other;
 53;
 (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
 Mismatches
 Example 2; Fig 2; 24pp; English
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BP.
AAA72621 standard; DNA; 530
 98US-0097616
 96US-0581529
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CCGCCCAGCTGCTGCCTGCCCACCAATTGACTCCCATCAGCATTCTATACATCGACGCG 1335
 CTGGAGTACGAGGCCTATCACTGCGAGGGTGTATGCGACTTCCCGCTGCGCTCGCACCTG 1215
 GAGCCCACCACCACGCCATCCATCCAGACGCTGATGAACTCCATGGACCCCGGCTCCACC 1275
 407
 467
 Oligo probe 3 (AAQ96214) designed on the basis of an amplified BMP-12
CTAGAGTACGAGGCCTATCACTGCGAGGCGTGTGCGACTTTCCGCTGCGCTCGCACTT
 408 CCGCCTAGCTGCTGCGTTCCCACCAAACTGACTCCCATTAGCATCCTGTACATCGACGCG
 morphogenetic protein; BMP-12; tendon; ligament; tendinitis;
 Σ
 compsn. for inducing tendon/ligament-like tissue formation
 Wolfman
 Bone morphogenetic proteins -12 and -13 and corresp. DNA
 Thomsen GH,
 Human bone morphogenetic protein (BMP)-12 DNA.
 Location/Qualifiers
 Rosen VA,
 Example; Page 73-75; 84pp; English
 AAQ96215 standard; DNA; 1345 BP
 94US-0333576.
93US-0164103.
94US-0217780.
 94WO-US14030
 /*tag= a
990..1301
/*tag= b
 (first entry)
 GENETICS INST INC. HARVARD COLLEGE.
 138..1301
 Melton DA,
 WPI; 1995-224320/29.
 P-PSDB; AAR78734
 1396 TAG 1398
 |||
| 528 TAG 530
 06-DEC-1994;
 02-NOV-1994;
07-DEC-1993;
 22-NOV-1995
 25-MAR-1994;
 AJ,
 mat_peptide
 WO9516035-A
 15-JUN-1995
 AAQ96215;
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 Wozney
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from
 1108
 1074
 1109 ACGTGAACTTCAAGGAGCTGGGCTGGGACGACTGGATTATCGCGCCCCTGGAGTACGAGG 1168
 CCTATCACTGCGAGGGTGTATGCGACTTCCCGCTGCGCTCGCACCTGGAGCCCACCAACC 1228
 954
 481
 643
 594
 763
 823
 714
 883
 774
 834
 894
 654
DNA sequence (AAQ96212) was radioactively labelled and used to
 Gaps
 screen a human genomic library. A positive clone was designated lambda-HuG-48. This bacteriophage was deposited under ATCC 75625 on Dec. 1993. The oligo hybridising region of this phage is localised to a 3.2 kb BamH1 fragment which was subcloned to PCR1-1#2 and deposited under ATCC 69517 on 7 Dec. 1993. The partial DNA sequence and derived As sequence of the 3.2 kb DNA insert of the plasmid subclone PCR1-1#2, derived from clone lamba-HuG-48 are shown in AAQ96207 and AAR78729 respectively. Additional DNA sequence of the 3.2 kb BamH1 insert of the plasmid PCR1-1#2 is given in AAQ96207 is contained in AAQ96215. As AAQ96215 is deerived fra a genomic clone it is difficult to determine the boundary between the 5' extent of coding sequence and the 3' limit of intervening
 704 CCTGGAAGCAGCTGTGCTTGGAGCTGCGGGCCGCATGGGGCGAGCTGGACGCCGGGGAGG
 835 TGGCCTCAGAGCCGCTGCCCGACCCAGGAACCGGCACCGCGTCGCCAAGGGCAGTCATTG
 524 AGCTGCGGCTCTTTCGCCAGGCGCCCTCAGCGCCCTGGGGGCCACCAGCCGGGCCGCTCC
 655 ececaegecaegeccegaeccegaeccearaecaeaecegecaeraegecraege
 715 CGGCGGAGGGGCCTCTGCGGCAGAGGGCGCGCGGTGCTAGTCGTCTCCTCCCGCACGC
 464 GACAGAAGTATTTGTTTGATGTGTCCATGCTCTCAGACAAGAAGAAGAGCTGGTGGGCGCGG
 584 ACGIGCAGCICITCCCTIGCCTTTCGCCCCTACTGCTGGACGCGCGGACCCTGGACCCGC
 ----GCCGTTGCTGCTGTCTGTCCACGTGCCCGGCCCCGACGCCCACGCCTGC
 TGTACTCGCGGGCAGCTGAGCCCCTAGTCGGTCAGCGCTGGGAGGCGTTCGACGTGGCGG
 824 TCGCCCGGAGGCTGCCGCCTCCCCAGGAGCGGCCCTGCTGGTGGTATTCACCAGATCCC
 895 GCGCCCCACACGCACGACGCCCTTGCCCCGCACCCGGACACCCCAGGCCAGCGCCC
 CCGAGGCGCGCGCGGGGACCCCAGCAACCGCCGCCCCCGGACCTGCGGAGTCTGGGGCT
 884 AGCGCA---AGAACCTGTTCGCAGAGATGCGCGAGCAGCTGGGCTCGGCCGAGGCTGC--
 -----GGCCCCGGGCGCGCGCCCGAGGGTCGTGGCCGCCGCCGTCGGGCCCCC
 GTCGCCATGGCAAGGCGCCACGCCAAGAAGTCCAGGCTACGCTGCAGCAAGAAGCCCCTGC
 Length 1345;
 24;
 Indels
 Sequence 1345 BP; 205 A; 447 C; 475 G; 218 T; 0 other;
 Score 259.2; DB 16;
Pred. No. 1.2e-37;
 378;
 0; Mismatches
 Query Match 18.2%;
Best Local Similarity 57.8%;
Matches 550; Conservative
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 1348
 This nucleotide sequence, designated v1-1, encodes a novel bone morphogenetic protein (see AAW25689), designated BMP-12. It was isolated from a human genomic library using a probe (see AAY90389) based on a partial BMP-12 sequence that had itself been identified using probes (see AAY90387-89) based on conserved regions in BMPs and TGF-beta proteins. A claimed method for inducing formation of tendon and/or ligament tissues involves the administration of a composition containing at least one protein selected from BMP-12, MP52 (see AAW26590) and BMP-13 (see AAW26591). The method is used for tissue (including skin) healing and repair. This is useful for
 MP-52
 ACGCCATCATCCAGACGCTGATGAACTCCATGGACCCCGGCTCCACCCCGCCCAGCTGCT
 GCGTGCCCACCAAATTGACTCCCATCAGCATTCTATACATCGACGCGGGCAATAATGTGG
 BMP-12; bone morphogenetic protein; human; tendon; ligament; wound healing; tissue repair; tendonitis; carpal tunnel syndrome;
 Inducing tendon and ligament formation using BMP-12, BMP-13 or M - useful for tissue healing and repair, treatment of tendonitis, improving fixation of tendons to bone etc
 TCTACAAGCAGTACGAGGACATGGTGGTGGAGTCGTGCGGCTGCAGGTAGCG 1400
 Wolfman NM;
 Thomsen GH,
 Human bone morphogenetic protein BMP-12 gene
 Example 1; Column 73-77; 43pp; English.
 Location/Qualifiers
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25-MAR-1994;
02-NOV-1994;
 Celeste AJ,
Wozney JM;
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 US5658882-A,
 22-DEC-1994;
 21-JAN-1998
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 mat_peptide
 19-AUG-1997
 AAT90390;
 therapy;
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 954
 Gaps
treating tendonitis, carpal tunnel syndrome and other defects of tranmatic or congenital origin, in cosmetic surgery and to improve fixation of tendons or ligaments to bone. The specified proteins can also be used to increase activity of other BMPs e.g. BMP-2
 GACAGAAGTATTTGTTTGATGTGTCTCCATGCTCTCAGACAAAGAAGAGCTGGTGGGCCGCGG
 524 AGCTGCGGCTCTTTCGCCAGGCGCCCTCAGCGCCCTGGGGGGCCACCAGCCGGGCCGCTCC
 535 TGTACTCGCGGCCAGCTGAGCCCCTAGTCGGTCAGCGCTGGGAGGCGTTCGACGTGGCGG
 CCGAGGCGCGCGCGCGGGGACCCCAGCAACCGCCCCCCGGACCTGCGGAGTCTGGGCT
 TCGGCCGGAGGGTGCGGCCTCCCCAGGAGCGGGCCCTGCTGGTGGTATTCACCAGATCCC
 AGCGCA - - - AGAACCTGTTCGCAGAGATGCGCGAGCAGCTGGGCTCGGCCGAGGCTGC - -
 ------GGGCCCGGGCGCGCGCGCCGAGGGGTCGTGGCCGCCGCCGCCGTCGGGCGCCCC
 835 TGCCTCAGAGCCGCTGCCCGACCCAGGAACCGGCACCGCGTCGCCAAGGGCAGTCATTG
 895 GCGCCCCCAGACGCAGAGGACGCCTTGGCCGGGACGCGCGCACGCCCAGGCCAGGCGCG
 1015 ACGTGGACTTCAAGGAGCTCGGCTGGACGACTGGATCATCGCGCCGCTGGACTACGAG
 CCTATCACTGCGAGGGTGTATGCGACTTCCCGCTGCGCTCGCACCTGGAGCCCACCAACC
 GCGTGCCCACCAAATTGACTCCCATCAGCATTCTATACATCGACGCGGGCAATAATGTGG
 ACGTGCAGCTCTTCCCTTTCGCCCCTACTGCTGGACGCGCGGGACCCTGGACCCCGC
 -----GCCGTTGCTGCTGTCCACGTGCCCGGGCGCCCCCGAGCGCCAACGCCTGC
 644 AGGGGGCGCCGCCGGCTGGGAAGTCTTCGACGTGTGGCAGGGCCTGCGCCACCAGC
 CCTGGAAGCAGCTGTGCTTGGAGCTGCGGGCCGCATGGGGCGAGCTGGACGCGGGGAGG
 CGGCCGAGGGGGCTCTGCGGCAGAGGAGCGCGCGGGGTGCTAGTCGTCTCCTCCCGCACGC
 CGGATGCCAGGCCTTGGCTGCCCTCGCCCGGCGCGCGGCGGCGCGCCACGGCCTTCGCCA
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 ACGCCATCATCCAGACGCTGATGAACTCCATGGACCCCGGCTCCACCCGCCCAGCTGCT
 DB 18; Length 1345;
 1349 TCTACAAGCAGTACGAGGACATGGTGGTGGAGTCGTGCGGCTGCAGGTAGCG 1400
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Pred. No. 1.2
 18.2%;
57.8%;
 Matches 550; Conservative
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 (see AAW26597).
 Query Match
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 1195
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Sequence 1345 BP; 205 A; 447 C; 475 G; 218 T; 0 other;
 Search completed: November 25, 2002, 01:08:17
 Query Match
 Matches
 464
 775
 1049
 1109
 1075
 704
 1169
 1229
 1289
 482
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 encoding a propertide from a member of the transforming growth factor (TGP) beta superfamily of proteins. This DNA is linked to a DNA sequence encoding an mature polypeptide consisting of Bone Morphogenetic Protein (BMP)-12, BMP-13 or MP52 protein. The DNA sequences are useful for producing proteins which induce tendon/ligament like tissue formation, and for isolating and cloning further DNA sequences encoding BMP-12 related proteins with similar activity. The proteins are useful for the induction of tendon/ligament-like tissue
 formation, wound healing, ligament and other tissue repair, augmenting the activity of bone morphogenetic proteins, and for treating tendonitis, carpal tunnel syndrome and other tendon and ligament defects. The present sequence is a DNA encoding human BMP-12 protein.
 New chimeric DNAs, useful for treating tendonitis, carpal tunnel syndrome and other tendon and ligament defects, comprises DNA encoding propeptide linked to DNA encoding bone morphogenetic proteins (BMP)-12 BMP-13 or MP52 -
 Human; bone morphogenic protein; BMP-12; vulnerary; antiinflammatory; analgesic; gene therapy; transforming growth factor-beta; TGF-beta; tissue formation; wound healing; tissue repair; ligament defect; carpal tunnel syndrome; tendonitis; ds.
 The invention relates to a chimeric DNA comprising a DNA sequence
Thomsen GH;
 "Human BMP-12 protein"
OS does not include start codon"
 Human bone morphogenic protein-12 (BMP-12) DNA #2.
 protein"
 Wolfman NM,
 "Mature BMP-12
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 94US-0362670
 93US-0164103
94US-0217780
 94US-0333576
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138..989
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P-PSDB; AAE10986.
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02-NOV-1994;
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 28-FEB-1997;
 22-DEC-1994;
07-DEC-1993;
 18-DEC-2001
 Celeste AJ,
Melton DA;
 sig_peptide
 mat_peptide
 04-SEP-2001
 AAD18337;
 HARD
 GEMY
 1255
 Homo
 RESULT 15
 Key
 AAD18337
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1048
 1108
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 894
 364 GCCAGAGCTTCCTGTTCGACGTGTCCAGCCTTAACGACGCAGACGAGGTGGTGGTGCTCC 423
 Gaps
 644 AGGGGGCGCCGCCGCCGCCGGCTGGGAAGTCTTCGACGTGTGGCAGGGCCTGCGCCACCAGC
 535 TGTACTCGCGGCAGCTGAGCCCCTAGTCGGTCAGCGCTGGGAGGCGTTCGACGTGGCGG
 CCTGGAAGCAGCTGTGCTTGGAGCTGCGGGCCGCATGGGGCCGAGCTGGACGCCGGGGAGG
 524 AGCTGCGGCTCTTTCGCCAGGCGCCCTCAGCGCCCTGGGGGGCCACCAGCCGGGCCGCTCC
 584 ACGIGCAGCICITCCCTTGCCTTTCGCCCCTACTGCTGGACGCGGGACCCTGGACCCGC
 -----GCGGTTGCTGCTGTCCACGTGCCCGGGCGCCCCGAGCGCCCACGCTGC
 CCGAGGCGCGCGCGCGGGGACCCCAGCAACCGCCGCCCCCGGGACCTGCGGAGTCTGGGCT
 655 GCGCAGTGGCAGGCCCGGTGCCGATGGCACTGCGGCGACTGGGCTTCGGCTGGC
 824 TCGCCCGGAGGGTGCGGCCTCCCCAGGAGCGGGCCCTGCTGGTGGTATTCACCAGATCCC
 AGCGCA----AGAACCTGTTCGCAGAGATGCGCGAGCAGCTGGGCTCGGCCGAGGCTGC--
 ------GGGCCCGGGCGCGCGCGCCGAGGGGTCGTGGCCGCCGCCGCCGTCGGGCGCCCC
 835 TGGCCTCAGAGCCGCTGCCCGACCCAGGAACCGGCACCGCGTCGCCAAGGGCAGTCATTG
 895 GCGGCCGCAGACGGAGGACGCCGTTGGCCGGGACGCGGACAGCGCAGGGCAGCGCG
 GTCGCCATGGCAAGCGCCACGCCAAGAAGTCCAGGCTACGCTGCAGCAGAAGCCCCTGC
 955 degececedecededecacadedececedadecececadececenadecearage
 ACGTGAACTTCAAGGAGCTGGGCTGGGACGACTGGATTATCGCGCCCCTGGAGTACGAGG
 1195 GIGIGCCAGGGGGCCTCAGCCTCAGCATCCTCTACATGGACGCCGCCAACAACGTIG
 GACAGAAGTATTTGTTTGATGTCCATGCTCTCAGACAAGAAGAAGAGCTGGTGGGCGCGG
 CCTATCACTGCGAGGGTGTATGCGACTTCCCGCTGCGCTCGCACCTGGAGCCCACCAACC
 ACGCCATCATCCAGACGCTGATGAACTCCATGGACCCCGGCTCCACCCCGGCCCAGCTGCT
 1135 ATGCCATCATTCAGACGCTGCTCAACTCCATGGCACCAGACGCGGCGCCGGCCTCCTGCT
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 24;
 22; Length 1345;
 1255 TCTACAAGCAATACGAGGACATGGTGGTGGAGGCCTGCGGCTGCAGGTAGCG 1306
 1349 TCTACAAGCAGTACGAGGACATGGTGGTGGAGTCGTGCGGCTGCAGGTAGCG 1400
 Indels
Score 259.2; DB 22;
Pred. No. 1.2e-37;
....+rhes 378;
 ;
 18.2%;
57.8%;
 Conservative
 Local Similarity
 550;
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Job time : 324 secs

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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

November 25, 2002, 02:52:20 ; Search time 51 Seconds (without alignments) 857.670 Million cell updates/sec Run on:

US-09-825-751A-20 2447 1 MDTPRVLLSAVFLISFLWDL......GNNVVYKQYEDMVVESCGCR 455 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 seqs, 96134422 residues Searched:

283224 hl number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR\_73:\*
1: pirl:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

|   | Description    |          | growth/differentia | bone morphogenetic | cartilage-derived | bone morphogenetic | SPDVR1 protein - s | bone morphogenetic | osteogenic protein |      | bone morphogenetic | bone morphogenetic | bone morphogenetic | bone morphogenetic | osteogenic protein | decapentaplegic pr | Vg-1-related prote | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
|   | DB ID          | 2 R55452 | JC23               | 2 S43294           |                   | 2 S43295           |                    |                    | ט                  |                    | щ                  | 2 149541           | U                  |                    |                    |                    | 2 JH0801           |                    | U)                 |                    | H                  | -                  |      |                    | A4914              | -                  |                    | JQ118              | 2 A26158           | A5479              |
|   | Length D       | 436      | 501                | 495                | 501               | 125                | 151                | 398                | 398                | 405                | 408                | 420                | 393                | 408                | 396                | 461                | 408                | . 394              | 408                | 452                | 353                | 402                | 454  | 401                | 400                | 426                | 431                | 430                | 588                | 510                |
| ф | Query<br>Match | 1 (**    | ~                  | 37.6               | 7                 | œ                  | ~                  | g                  | g,                 | æ                  | æ                  | 7                  | 7                  | 17.7               | 17.6               | 7                  | 7.                 |                    | 17.1               |                    |                    |                    | 17.0 |                    |                    | 16.6               |                    | •                  | 16.2               |                    |
|   | Score          | 1798     | 927.5              | 919.5              | 918.5             | 691                | 549                | 470                | 464                | S                  | 41                 |                    | m                  | 432.5              |                    |                    |                    | $\sim$             | 419.5              | 18.                |                    |                    |      |                    | 408.5              | 407                | 401.5              | 401                | 395.5              | σ.                 |
| ) | Result<br>No.  | -        | 1 73               | m                  | 4                 | 2                  | 9                  | 7                  | 89                 | O                  | 10                 | 11                 | 12                 | 13                 | 14                 | 15                 | 16                 | 17                 | 18                 | 19                 | 20                 | 21                 | 22   | 23                 | 24                 | 25                 | 56                 | 27                 | 28                 | 29                 |

| bone morphogenetic gene nodal protein gene nodal protein TGF beta homolog d bone morphogenetic cet.1 protein - Ca TGF-beta-related p vgr protein - rat bone morphogenetic vgr protein - rat bone morphogenetic Vgl embryonic grinhibin beta-A cha inhibin beta-A cha |  |
|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--|
| BMHU6<br>25218<br>440735<br>74646<br>704646<br>704838<br>74286<br>A43918<br>837618<br>BMHU3<br>A29619<br>C39364<br>B47072<br>WFPGBA<br>S50898                                                                                                                                                                                                                       |  |
| пноновновновни                                                                                                                                                                                                                                                                                                                                                      |  |
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| 0 1 1 2 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3                                                                                                                                                                                                                                                                                                                           |  |

## ALIGNMENTS

| Σ b                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |                                                                                                                                                                          |                                                                |                                                                         |                                                                         | *                                                                       |                                                                   |                                                                         |                                                                          |                                |
|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------|-------------------------------------------------------------------------|-------------------------------------------------------------------------|-------------------------------------------------------------------------|-------------------------------------------------------------------|-------------------------------------------------------------------------|--------------------------------------------------------------------------|--------------------------------|
| V.J.P.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | 8;                                                                                                                                                                       |                                                                |                                                                         |                                                                         | :'                                                                      |                                                                   |                                                                         |                                                                          |                                |
| RESULT 1 B55452 cartilage-derived morphogenetic protein 2 precursor - bovine (fragment) cartilage-derived morphogenetic protein 2 precursor - bovine (fragment) C; Species: Bos primigenius taurus (cattle) C; Date: 10-Feb-1995 #sequence_revision 10-Feb-1995 #text_change 26-May-2000 C; Accession: B55452 R; Chang, S.C.; C.; Hoang, B.; Thong, B.; Tyoukicevic, S.; Luyten, F.P.; Ryba, N.J.P.; A; Title: Cartilage-derived morphogenetic proteins. New members of the transforming A; Reference number: A55452; MUID:95050604; PMID:7961761 A; Accession: B55452 A; Status: preliminary; not compared with conceptual translation A; Molcoule type: mRNA A; Residues: 1-436 cCHA> A; Residues: 1-436 cCHA> A; Residues: GB:U13661; NID:9632489; PIDN:AAA61416.1; PID:9632490 C; Superfamily: Inhibin | Query Match 73.5%; Score 1798; DB 2; Length 436;<br>Best Local Similarity 80.8%; Pred. No. 8.1e-120;<br>Matches 354; Conservative 18; Mismatches 48; Indels. 18; Gaps 8; | 33 SSAELGSTKGWRSRKEGKMQRAPRDSDAGREGQEPQPRPQDEPRAQQPRAQEPP 86 : | 97 GRGPRVVPHEYMLSIYRTYSIAEKLGINASFFQSSKSANTITSFVDRGLDDLSHTPLRRQ 146<br> | 147 KYLFDVSMLSDKEELVGAELRLFRQAPSAPWGPPAGPLHVQLFPCLSPLLDARTLDPQG 206<br> | 207 APPAGWEVEDVWQGLRHQPWKQLCLELRAAW-GELDAGEAEARARGPQQPPPDLRSIGF 265<br> | 266 GRRVRPPQERALLVVFTRSORKNLFAEMREQLGSA-EAAGPGAGAEGSWPPPS 317<br> | 318 GAPDARPWLPSPGRRRRTAFASRHGKRHGKKSRLRCSKKPLHVNFKELGWDDWIIAPLE 377<br> | 378 YEAYHCEGVCDFPLRSHLEPTNHAIIQTLMNSMDPGSTPPSCCVPTKLTPISILYIDAGN 437<br> | 438 NVVYKQYEDNVVESCGCR 455<br> |
| RESULT<br>855452<br>cartila<br>C;Speci<br>C;Date:<br>C;Acces<br>C;Acces<br>R;Chang<br>J; Biol<br>A;Refer<br>A;Refer<br>A;Refer<br>A;Resic<br>A;Resic<br>A;Resic<br>A;Resic<br>A;Resic<br>A;Resic<br>A;Resic<br>A;Resic<br>A;Resic<br>A;Resic<br>A;Resic<br>A;Resic<br>A;Resic<br>A;Resic<br>A;Resic<br>A;Resic                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | Query<br>Best<br>Match                                                                                                                                                   | yo<br>da                                                       | Oy<br>Db                                                                | Oy 1.                                                                   | Qy 2<br>Db 1                                                            | Oy 2<br>Db 2                                                      | Qy 3:                                                                   | Oy 3.                                                                    | Oy 4<br>Db 4                   |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |                                                                                                                                                                          |                                                                |                                                                         |                                                                         |                                                                         |                                                                   |                                                                         |                                                                          |                                |

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 Query Match 37.6%
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Matches 209; Conservative
 A;Cross-references: GDB:438940
C;Superfamily: inhibin
 A; Gene: GDB: CDMP1
 207;
 R 455
 R 495
 Query Match
Best Local &
 C;Genetics:
 276
 335
 Matches
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 C; Species: Mus musculus (house mouse)
C;Date: 20-oct: 1994 #sequence_revision 10-Nov-1995 #text_change 17-Mar-2000
C;Accession: S43294
R;Storm, E.E.; Huynh, T.V.; Copeland, N.G.; Jenkins, N.A.; Kingsley, D.M.; Lee, S.J.
Nature 368, 639-643, 1994
A;Title: Limb alterations in brachypodism mice due to mutations in a new member of the A;Reference number: S43294; MUID:94195427; PMID:8145850
A;Accession: S43294
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R: Hoetten, G: Neidhardt, H.; Jacobowsky, B.; Pohl, J.
R: Hoetten, G: Neidhardt, H.; Jacobowsky, B.; Pohl, J.
B: Biochem. Biophys. Res. Commun. 204, 646-652, 1994
A: Title: Cloning and expression of recombinant human growth/differentiation factor. A: Reference number: JC2347; MUID: 95071375; PMID: 7980526
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A: Molecule type: DNA
A: Residues: 1-501 <HOE>

 16;
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 37.9%; Score 927.5; DB 2;
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 Gene: GDB:BMP9
 Introns: 211/1
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 Genetics
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C;Date: 10-Feb-1995 #sequence\_revision 10-Feb-1995 #text\_change 17-Mar-2000
C;Date: 10-Feb-1995 #sequence\_revision 10-Feb-1995 #text\_change 17-Mar-2000
C;Accession: A5545 #sequence\_revision 10-Feb-1995 #text\_change 17-Mar-2000
C;Accession: A5545 #sequence\_revision 10-Feb-1995 #text\_change 17-Mar-2000
J; Biol. Chem. 269, 28227-28234, 1994
A;Title: Cartilage-derived morphogenetic proteins. New members of the transforming cartilage-derived morphogenetic proteins. 18; 15; 60 PGGHIYGVGATNARAK-GSSGQTQAKKDEPRKMPPRSG-----GSETKPGPSSQTRQAAA 113 217 VWQGLRH-QPWKQLCLELRAAWGELDAGEAEARARGPQQPPPPDLRSLGFGRRVRPPQER 275 YSIAEKLGINASFFQSSKSANTITSFVDRGLDDLSHTPLRRQKYLFDVSMLSDKEELVGA 164 290 IWKLFRNFKNSAQLCLELE-AW---ERGRA-------VDLRGLGFERTARQVHEK 333 ALLVVFTRSQRKNL-FAEMREQLGSAEAAGPGAGAEGSWPPPSGAPDARPWLPSPGRRRR 334 RTAFASRHGKRHGKKSRLRCSKKPLHVNFKELGWDDWIIAPLEYEAYHCEGVCDFPLRSH 394 LEPTNHAIIQTLMNSMDPGSTPPSCCVPTKLTPISILYIDAGNNVVYKQYEDMVVESCGC 454 -- 79 PID:9488462 21 PGFQQASISSSCSSAELGSTKGMRSRKEGKMQRAPRDSDAGREGQEPQPRPQDE----ELRLFRQAP - - - SAPWGPPAGPL-HVQLFPCLS - - - - PLLLDARTLDPQGAPPAGWEVFD 91; 95; 501; Length 495; Indels Length A;Molecule type: mRNA A;Residues: 1.495 <STVO> A;Cross rreferences: GB:U08337; NID:g488461; PIDN:AAA18778.1; C;Superfamily: inhibin cartilage-derived morphogenetic protein 1 precursor - human A;Molecule type: mRNÅ A;Residues: 1-501 <CHA> A;Cross-references: GB:U13660; NID:g600731; PID:g600732 37.6%; Score 919.5; DB 2; 43.5%; Pred. No. 1.3e-57; tive 74; Mismatches 107; 1 37.5%; Score 918.5; DB 2; Similarity 44.3%; Pred. No. 1.5e-57; Onservative 64; Mismatches 101;

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•• Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

|           | Description              | Sequence 26, Appl |                   |                  | Sequence 26, Appl  | Sequence 32, Appl | Sequence 32, Appl | 32,              | 32,                | 2.               | 10               | 10,              | 10,               | 3,               | m                | Sequence 34, Appl | 34                | 34,              | 34,                | Sequence 6, Appli | Sequence 6, Appli | Sequence 6, Appli | 5                | 7                | 2               | 7                 | 7,               | 7,              |
|-----------|--------------------------|-------------------|-------------------|------------------|--------------------|-------------------|-------------------|------------------|--------------------|------------------|------------------|------------------|-------------------|------------------|------------------|-------------------|-------------------|------------------|--------------------|-------------------|-------------------|-------------------|------------------|------------------|-----------------|-------------------|------------------|-----------------|
| SUMMAKIES | ID                       | US-08-362-670B-26 | US-08-333-576C-26 | US-08-808-324-26 | PCT-US94-14030A-26 | US-08-362-670B-32 | US-08-333-576C-32 | US-08-808-324-32 | PCT-US94-14030A-32 | US-08-288-508C-2 | US-08-455-559-10 | US-09-145-060-10 | PCT-US94-00657-10 | US-08-289-222E-3 | US-09-054-526B-3 | US-08-362-670B-34 | US-08-333-576C-34 | US-08-808-324-34 | PCT-US94-14030A-34 | US-08-581-529B-6  | US-09-097-616-6   | PCT-US94-07762-6  | US-08-362-670B-2 | US-08-333-576C-2 | US-08-808-324-2 | PCT-US94-14030A-2 | US-08-581-529B-7 | US-09-097-616-7 |
|           | DB                       | -                 | ٣                 | 4                | 5                  | 7                 | т                 | 4                | 5                  | 7                | 7                | 4                | 2                 | ٣                | 4                | П                 | e                 | 4                | 'n                 | ٦                 | ო                 | Ŋ                 | -1               | m                | 4               | Ŋ                 | ٦                | ٣               |
|           | Query<br>Match Length DB | 321               | 321               | 321              | 321                | 263               | 263               | 263              | 263                | 501              | 495              | 495              | 495               | 401              | 401              | 388               | 388               | 388              | 388                | 134               | 134               | 134               | 294              | 294              | 294             | 294               | 119              | 119             |
| ø         | Query<br>Match           | 71.4              | 71.4              | 71.4             | 71.4               | 49.1              | 49.1              | 49.1             | 49.1               | 37.9             | 37.6             | 37.6             | 37.6              | 37.5             | 37.5             | 31.3              | 31.3              | 31.3             | 31.3               | 29.9              | 29.9              | 29.9              | 28.3             | 28.3             | 28.3            | 28.3              | 27.0             | 27.0            |
|           | Score                    | 1747              | 1747              | 1747             | 1747               | 1202.5            | 1202.5            | 1202.5           | 1202.5             | 927.5            | 919.5            | 919.5            | 919.5             | 917.5            | 917.5            | 765               | 765               | 765              | 765                | 731               | 731               | 731               | 691.5            | 691.5            | 691.5           | 691.5             | 661              | 661             |
|           | Result<br>No.            | 1                 | 7                 | m                | 4                  | Ŋ                 | φ                 | 7                | œ                  | σ                | 10               | 11               | 12                | 13               | 14               | 15                | 16                | 17               | 18                 | 19                | 20                | 21                | 22               | 23               | 24              | 25                | 26               | 27              |
|           |                          |                   |                   |                  |                    |                   |                   |                  |                    |                  |                  |                  |                   |                  |                  |                   |                   |                  |                    |                   |                   |                   |                  |                  |                 |                   |                  |                 |

| Sequence 7, Appli<br>Sequence 28, Appl<br>Sequence 28, Appl<br>Sequence 28, Appl<br>Sequence 30, Appl<br>Sequence 30, Appl<br>Sequence 30, Appl<br>Sequence 30, Appl<br>Sequence 6, Appli<br>Sequence 6, Appli | Sequence 13, Appl<br>Sequence 13, Appl<br>Sequence 4, Appli<br>Sequence 4, Appli<br>Sequence 4, Appli<br>Sequence 4, Appli |
|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------|
| PCT-US94-07762-7<br>US-08-362-670B-28<br>US-08-333-576C-28<br>US-08-324-28<br>PCT-US94-14030A-28<br>US-08-362-670B-30<br>US-08-333-576C-30<br>US-08-808-124-30<br>US-08-81-528A-6<br>PCT-US94-14030A-30<br>US-08-581-528A-6<br>PCT-US94-07799-6<br>US-08-455-559-13                                                                          | US-09-145-060-13 PCT-US94-00657-13 US-08-36-670B-4 US-08-333-576C-4 US-08-808-324-4                                        |
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|                                                                                                                                                                                                                                                                                                                                              | 4 4 4 4 4 4<br>0 4 6 6 7                                                                                                   |

## ALIGNMENTS

|          | on US/08362670B                                                              | Anthony J.                                                 | John      | Vicki A.                 |          | $\Box$ | Η          | 37.                     | CS INSTITUTE, INC.    | dgePark Drive | . (               | יררא<br>מרובא            |    | )RM: | ppy disk | IBM PC compatible |    | Patentin Release #1.0, Version #1.25 | DAIA:               | : 03/06/302/0/0B<br>mber 22, 1994 | 14                    | MATION:  | PZ,                     | :K: 32,618<br>            | P                       | 498-8260                |                        | NO: 26:                      | 11.C3:    |            |         | ein                                        | 71.4%; Score 1747; DB 1; Length 321; 100.0%; Pred. No. 4.3e-141; | O. Mismatch               |
|----------|------------------------------------------------------------------------------|------------------------------------------------------------|-----------|--------------------------|----------|--------|------------|-------------------------|-----------------------|---------------|-------------------|--------------------------|----|------|----------|-------------------|----|--------------------------------------|---------------------|-----------------------------------|-----------------------|----------|-------------------------|---------------------------|-------------------------|-------------------------|------------------------|------------------------------|-----------|------------|---------|--------------------------------------------|------------------------------------------------------------------|---------------------------|
| RESULT 1 | US-08-362-670B-26; Sequence 26, Application US/08362670B; Patent No. 5658882 | <pre>; GENERAL INFORMATION: ; APPLICANT: Celeste. Ar</pre> | Wozney, J | ) APPLICANT: Rosen, Vic) | Thomsen, | . 🖰    | INVENTION: | CORRESPONDENCE ADDRESS: | ; ADDRESSEE: GENETICS | <u></u>       | ; CITY: Cambridge | CONTINUEY: HASSACHUSELLS | 17 | 15   | щ        |                   | C) | ; SOFTWAKE: Patentin Rel             | . ADDITORATION DATE | ; FILING DATE: December 22, 1994  | ; CLASSIFICATION: 514 | /AGENT I | ; NAME: Lazar, Steven R | * REGISTRATION NUMBER: 32 | TELECOMMUNICATION INFOR | ; TELEPHONE: 617 498-82 | ; TELEFAX: 617 876-585 | ; INFORMATION FOR SEQ ID NO: | 321 amino | amino acid | CGY: 15 | ; MOLECULE TYPE: protein US-08-362-670B-26 | nilarity                                                         | Watchen 210. Concernation |

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SGAPDARPWLPSPGRRRRTAFASRHGKRHGKKSRLRCSKKPLHVNFKELGWDDWIIAPL 376
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TELEFAX: 61
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 COUNTRY:
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 Length 321;
 TITLE OF INVENTIONS
CORRESPONDENCE: 37
CORRESPONDENCE: 37
STREE: GENETIONS
STREES
 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/333,576C
 Mismatches
 Score 1747;
Pred. No. 4
 FILING DATE: No. 6027919ember 2, 1994 CLASSIFICATION: 435
 E: GENETICS INSTITUTE, INC. 87 CambridgePark Drive
 ATTORNEY/AGENT INFORMATION:
NAME: Lazar, Steven R.
REGISTRATION NUMBER: 32,618
REFERENCE/DOCKET NUMBER: 5202-B
TELEPHONE: 617 498-8260
TELEPHONE: 617 498-8260
 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 Sequence 26, Application US/08333576C
Patent No. 6027919
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100.08; Pre
0;
 T: Celeste, Anthony J.
T: Wozney, John
T: Rosen, Vicki A.
T: Wolfman, Neil
T: Thomsen, Gerald H.
 NNVVYKQYEDMVVESCGCR 455
 LENGTH: 321 amino acids TYPE: amino acid
 Query Match 71.4
Best Local Similarity 100.
Matches 319; Conservative
 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
 CITY: Cambridge
STATE: Massachusetts
 MOLECULE TYPE: protein US-08-333-576C-26
 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
 GENERAL INFORMATION:
APPLICANT: Celest
APPLICANT: Wozney
 USA
 02140
 RESULT 2
US-08-333-576C-26
 APPLICANT:
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; Mismatches 0.
 APPLICANT: Celeste, Anthony J.
APPLICANT: Wozney, John
APPLICANT: Wozney, John
APPLICANT: Wolfman, Neil
APPLICANT: Thomsen, Gerald H.
APPLICANT: Melton, Douglas A.
TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
 PatentIn Release #1.0, Version #1.25
 Query Match 71.4%; Score 1747; Best Local Similarity 100.0%; Pred. No. 4 Matches 319; Conservative 0; Mismatche
 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/808,324
FILING DATE: Herewith
CLASSIFICATION: 514
 ADDRESSEE: GENETICS INSTITUTE, STREET: 87 CambridgePark Drive
Sequence 26, Application US/08808324 Patent No. 6284872
 COMPUTER: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/AssortWARE: Patert
 REFERENCE/DOCKET NUMBER: 5: TELECOMMUNICATION INFORMATION
 ATTORNEY/AGENT INFORMATION:
 : 321 amino acids
amino acid
 NAME: Lazar, Steven R. REGISTRATION NUMBER: 3
 INFORMATION FOR SEQ ID NO:
 617 876-5851
 SEQUENCE CHARACTERISTICS
LENGTH: 321 amino aci
 Cambridge
: Massachusetts
 ; MOLECULE TYPE: protein US-08-808-324-26
 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
 GENERAL INFORMATION:
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